



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 143545

TO: Vanessa L Ford
Location: REM/3B25/3C18
Art Unit: 1645
Friday, January 28, 2005

Case Serial Number: 10/017168

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Ford,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

From: Chan, Christina
Sent: Thursday, January 27, 2005 3:16 PM
To: Ford, Vanessa; STIC-Biotech/ChemLib
Subject: RE: In re: 10/017168 sequence search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Ford, Vanessa
Sent: Thursday, January 27, 2005 1:40 PM
To: Chan, Christina
Subject: In re: 10/017168 sequence search

Please search the SEQ ID NOs: 2, 9, 11, 12, 13, 14, 15, 16, 17 and 18. Please include interferences. Please rush.

Vanessa L. Ford
Biotechnology Patent Examiner
Office: REM 3B25
Mailbox: REM 3C18
Phone: 571.272.0857
Art Unit:1645

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JAN 27 2005
STIC

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 1/28/05
Date Completed: 1/28/05
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # 10
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: QSP
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 / Search time 379.116 Seconds
(without alignments)
655.635 Million cell updates/sec

Title: US-10-017-168-2
Perfect score: 2188
Sequence: 1 MFVRSDFPKNTAVEISNLE.....HTKQSHSVSNAPNQRKP 432

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: uniprot_sprotc:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2188	100.0	432	051953	051953 treponema p
2	2178	99.5	548	093CA4	093CA4 treponema p
3	1478	67.4	428	09ALV6	09ALV6 treponema p
4	1286.5	58.8	393	093CA3	093CA3 treponema p
5	1043.5	47.7	348	09ALV7	09ALV7 treponema p
6	967	44.2	256	083448	083448 treponema p
7	478.5	21.9	227	083449	083449 treponema p
8	368.5	16.8	458	073NG7	073NG7 treponema d
9	285	13.0	1108	AA511704	AA511704 treponema
10	285	13.0	1108	09ND10	09ND10 babesia big
11	279	12.8	5458	09U459	09U459 plasmodium
12	268	12.2	2768	09VC00	09VC00 drosophila
13	267.5	12.2	432	0964C9	0964C9 encephalito
14	267.5	12.2	721	YCF2_OENPI	YCF2_OENPI
15	264.5	12.1	843	06GLM0	06GLM0 xenopus lae
16	264.5	12.1	897	013098	013098 xenopus lae
17	260	11.9	913	013099	013099 xenopus lae
18	260	11.9	913	06DDC0	06DDC0 xenopus lae
19	260	11.9	1110	091255	091255 petromyzon
20	256	11.7	466	06NE60	06NE60 magnetospor
21	256	11.7	474	CAE12033	CAE12033 magnetosp
22	255.5	11.7	474	0942K8	0942K8 oryza sativ
23	255.5	11.7	567	09HD28	09HD28 homo sapien
24	254.5	11.6	248	09LRH2	09LRH2 leishanus ba
25	252.5	11.5	1167	Q7SH94	Q7SH94 neurospora
26	251.5	11.5	1394	CMG4_BOVIN	CMG4_BOVIN
27	249.5	11.4	572	08MKF9	08MKF9 canis famli
28	248.5	11.4	3455	06R5A9	06R5A9 tenebrio mo
29	248.5	11.4	3455	AA897872	AA897872 tenebrio
30	248	11.3	1070	08LYT0	08LYT0 bacillus an
31	248	11.3	1070	AA29649	AA29649 bacillus

ALIGNMENTS

RESULT 1	PRELIMINARY;	PRT;	432 AA.
051953			
ID 051953			
AC 01-JUN-1998 (TREMBLrel. 06, Created)			
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE Acidic repeat protein.			
OS Treponema pallidum.			
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX NCBI_TaxID=160;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=Nichols;			
RA Steiner B.M., Liu H., Rodas B.;			
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AF015824; AAB94541.1; -			
SQ SEQUENCE 432 AA; 46364 MW; 8FE1E4C5CE46A23 CRC64;			
Query Match	100.0%;	Score 2188;	DB 2; Length 432;
Best Local Similarity	100.0%;	Pred. No. 4, 2e-104;	
Matches 432;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY 1 MFVRSDFPKNTAVEISNLEKNAQAQAVVIGHAGIPGLVSLAPAAQAQIGVYQAVRV 60			Q26893 trypanosoma
1 MFVRSDFPKNTAVEISNLEKNAQAQAVVIGHAGIPGLVSLAPAAQAQIGVYQAVRV 60			Q73CU8 bacillus ce
QY 61 RVVTLGTVRGSGTSDGSLASLPSRVPARPQRPPLSPGHTVPEYRDVTFDDPR 120			AA839897 bacillus
61 RVVTLGTVRGSGTSDGSLASLPSRVPARPQRPPLSPGHTVPEYRDVTFDDPR 120			Q6PCS2 brachydanio
QY 121 LVSPLEREVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE 180			AAH59189
121 LVSPLEREVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE 180			Q26892 trypanosoma
QY 181 EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE 240			Q26892 trypanosoma
181 EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE 240			Q26892 trypanosoma
QY 241 EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE 300			Q801T3 xenopus lae
241 EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE 300			Q80BK7 saimiriine
QY 301 EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE 360			Q7RMK1 plasmodium
301 EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE 360			Q81HN3 plasmodium
QY 361 EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE 420			Q80AG4 saimiriine
361 EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE 420			Q9DG11 fugu rubrip
QY 421 VNSAPNQRKP 432			Q96214 encephalito
421 VNSAPNQRKP 432			
QY 421 VNSAPNQRKP 432			
421 VNSAPNQRKP 432			
DB 421 VNSAPNQRKP 432			

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OM protein - protein search, using SW model

Run on: January 28, 2005, 11:05:24 ; Search time 67.3068 Seconds
(without alignments)
617.555 Million cell updates/sec

Title: US-10-017-168-2

Perfect score: 2188
Sequence: 1 MFVRSDFMPKNTAVEISNLE.....HTKQPSHSVSNAPNQFRKP 432

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	967	44.2	256	2 F71326	hypothetical prote
2	478.5	21.9	227	2 G71326	hypothetical prote
3	267.5	12.2	721	2 S29795	hypothetical prote
4	260	11.9	913	2 T52485	neurofilament prot
5	260	11.9	1110	2 I51116	NE-180 - sea lamp
6	249	11.4	590	2 A40437	glutamic acid-rich
7	243	11.1	391	2 S27850	surface antigen Tc
8	242.5	11.1	1271	2 A45555	glutamate rich pro
9	228	10.4	1094	2 S49313	protein kinase - B
10	225.5	10.3	630	2 S29796	hypothetical prote
11	224.5	10.3	2109	2 E89066	protein H05009.1 l
12	224.5	10.3	2109	2 T33247	hypothetical prote
13	224	10.2	845	2 A45669	neurofilament trip
14	220.5	10.1	407	1 EDBEQ3	immediate-early pr
15	211	9.6	296	2 A54527	110k antigen - pla
16	210.5	9.6	506	2 S47439	I2 protein - Trypa
17	210.5	9.6	849	2 S00030	neurofilament trip
18	210	9.6	679	2 S55395	neurofilament prot
19	206	9.4	679	2 S28366	recombination repa
20	206	9.4	1560	2 T30282	calcium-binding pr
21	204	9.3	7962	2 I38346	elastic titin - hu
22	203	9.3	1621	2 A82255	hypothetical prote
23	200.5	9.2	1881	2 H95076	zinc metalloprotei
24	197.5	9.0	916	2 A27864	neurofilament trip
25	195.5	8.9	544	1 I36911	involucrin L - dou
26	195.5	8.9	798	2 I50479	neurofilament medi
27	195	8.9	699	2 T01029	hypothetical prote
28	191	8.7	924	2 S27923	gene Lf3 protein -
29	189	8.6	387	2 D84885	hypothetical prote

30	189	8.6	1262	2 T22523	hypothetical prote
31	188	8.6	837	2 T02761	cuter arm dynein 1
32	187.5	8.6	450	1 C29413	ubiquinol-cytochro
33	187	8.5	880	2 D89756	protein T23B7.2b (
34	186	8.5	518	2 G84488	fn/spm-like transp
35	185	8.5	1187	2 U03316	hypothetical 125k
36	184.5	8.4	784	2 P00009	neurofilament trip
37	184	8.4	706	2 A45990	junctional sarcopl
38	183	8.4	2722	2 T20532	hypothetical prote
39	183	8.4	2738	2 E88320	protein F07A11.6 (
40	182	8.3	333	2 T10738	hypothetical prote
41	182	8.3	699	2 E84565	hypothetical prote
42	182	8.3	754	2 AC2807	ompa family protei
43	182	8.3	754	2 B97586	hypothetical prote
44	180	8.2	1020	1 QP0UH	neurofilament trip
45	180	8.2	5170	2 T15348	hypothetical prote

ALIGNMENTS

RESULT 1

hypothetical protein TP0433 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: F71326

R/Faaser, C.M.; Norris, S.J.; Weinsrock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; McI
rean, U.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McI
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; PMID:98332770; PMID:9665876

A/Accession: F71326

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-256 <COL>

A/Cross-references: UNIPROT:O83448; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AA0654

A/Experimental source: strain Nichols

C/Genetics:

A/Genes: TP0433

Query Match 44.2%; Score 967; DB 2; Length 256;
Best Local Similarity 99.0%; Pred. No. 3.8e-45;
Matches 193; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MFVRSDFMPKNTAVEISNLEKNAKAQAVVTGAGIPGLIVSLAPPAQAQGLGVQAVRV	60
DB	57	MFVRSDFMPKNTAVEISNLEKNAKAQAVVTGAGIPGLIVSLAPPAQAQGLGVQAVRV	116
QY	61	RVRTTGTVGSGSOTSDGLSLASLPSPVPAPAPADPLSSPPAGHTVPEYRDTVPFDDPR	120
DB	117	RVRTTGTVGSGSOTSDGLSLASLPSPVPAPAPADPLSSPPAGHTVPEYRDTVPFDDPR	176
QY	121	LVSPISREVEDAPKVEPASERGGERVEDAPKVEPASERGGERVEDAPKVEPAS	180
DB	177	LVSPISREVEDAPKVEPASERGGERVEDAPKVEPASERGGERVEDAPKVEPAS	236
QY	181	EREGREREVEDAPKV 195	
DB	237	EREGREREVEDAPKV 251	

RESULT 2

hypothetical protein TP0434 - syphilis spirochete

C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: G71326

R/Faaser, C.M.; Norris, S.J.; Weinsrock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; McI
rean, U.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McI
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 409.335 Seconds
(without alignments)
378.592 Million cell updates/sec

Title: US-10-017-168-2

Perfect score: 2188
Sequence: 1 MFVSDMFPKNTAVEISNLE.....HTKOPSHSVSNAPNQRKP 432

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003s:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2188	100.0	432	4	AA848316
2	1480	67.6	312	4	AA848318
3	1048	47.9	232	4	AA848317
4	268	12.2	2768	4	ABB68397
5	255.5	11.7	567	4	AAE13147
6	254.5	11.6	1000	6	ABJ25647
7	249.5	11.4	522	4	AAE02397
8	245	11.2	1018	2	AA898747
9	245	11.2	1018	2	AA898747
10	245	11.2	1018	8	AA898747
11	245	11.2	1018	8	AA898747
12	244.5	11.2	412	2	AAW03626
13	244.5	11.2	902	4	AA829778
14	241	11.0	360	2	AAW03627
15	240.5	11.0	783	2	AA805804
16	229	10.5	552	7	ADC31182
17	229	10.5	1388	7	ABJ38696
18	225.5	10.3	1388	7	ABJ38696
19	224	10.2	845	6	ABJ69333
20	223.5	10.2	864	4	AAW04614
21	216.5	9.9	489	4	AAW039026
22	214.5	9.8	382	4	AB858655
23	213.5	9.8	611	2	AAE02399
24	213.5	9.8	611	4	AAU29039
25	213.5	9.8	611	4	AAU25510
				7	ADG17131

26	206	9.4	553	7	ADM05820	Adm05820 Human pro
27	205.5	9.4	474	8	ADN46475	Adn46475 Thermoco
28	205	9.4	869	7	AD160170	Ad160170 Secreted
29	204	9.3	293	4	AAE02398	AAE02398 Canine re
30	204	9.3	486	5	AAE23036	AAE23036 Human thl
31	204	9.3	679	4	AB859691	AB859691 Drosophill
32	202	9.2	385	6	ABU20070	Abu20070 Protein e
33	200.5	9.2	565	2	AAW61247	AAW61247 Streptoco
34	200.5	9.2	565	5	ABP54665	ABP54665 S. pneumo
35	200.5	9.2	565	7	ADC45299	ADC45299 S. pneumo
36	200.5	9.2	1245	6	ABP56885	ABP56885 Staphyloc
37	200.5	9.2	1881	3	AAV44506	AAV44506 Streptoco
38	200.5	9.2	1881	6	ABU01047	Abu01047 S. pneumo
39	200.5	9.2	1881	8	ADM92119	Adm92119 S. pneumo
40	200.5	9.2	2397	6	ABU43308	Abu43308 Protein e
41	200	9.1	654	4	AB863266	AB863266 Drosophill
42	200	9.1	688	4	AB863269	AB863269 Drosophill
43	199	9.1	546	6	ABP56886	ABP56886 Staphyloc
44	198	9.0	259	1	AAV40376	AAV40376 Sequence
45	197.5	9.0	554	2	AAV20763	AAV20763 Human neu

ALIGNMENTS

RESULT 1
ID AAB48316
X X AAB48316 standard; protein; 432 AA.
X X
X X AAB48316;
X X
X X 11-SEP-2003 (revised)
X X 20-APR-2001 (first entry)
X X
X X T. pallidum esp. pallidum (N1) acidic repeat protein (arp).
X X Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
X X yaws; bejel.
X X
X X Treponema pallidum; esp. pallidum.
X X
X X W0200077486-A2.
X X
X X 21-DEC-2000.
X X
X X 14-JUN-2000; 2000WO-US016425.
X X
X X 14-JUN-1999; 99US-0138981P.
X X
X X (USSH) US DEPT HEALTH & HUMAN SERVICES.
X X
X X Liu H, Steiner B, Rhodes B;
X X WPI; 2001-080711/09.
X X N-PSDB; AAC84647.
X X
X X Detecting Treponema pallidum in blood, saliva, etc., by detecting
X X formation of a complex between immunogenic peptides of acidic repeat
X X protein of the bacterium and an antibody present in the biological
X X sample.
X X
X X Claim 15; Fig 6; 73p; English.
X X
X X The invention relates to a method of detecting presence of Treponema
X X pallidum (Tp), anti-treponemal antibodies (Abs), or both in a biological
X X sample that involves contacting an acidic repeat protein (arp), or one or
X X more isolated immunogenic TP peptides of arp with an Ab containing
X X biological sample and then detecting the formation of a complex between
X X immunogenic peptides and Ab. The presence of the complex indicates the
X X presence of TP. The method is thus useful for diagnosing syphilis, yaws,
X X and bejel diseases. The immunogenic peptides or the Abs raised against
X X arp, as part of an immunogenic composition, are useful for inducing a
X X protective immune response against syphilis, yaws or bejel caused by TP.

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 ; Search time 17.5517 Seconds
(without alignment)

655.635 Million cell updates/sec

Title: US-10-017-168-9
Perfect score: 101
Sequence: 1 PKVPEPASERGEGEREVEDA 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	101	100.0	256	083448	083448 treponema p
2	101	100.0	432	051953	051953 treponema p
3	101	100.0	548	093CA4	093CA4 treponema p
4	97	96.0	227	083449	083449 treponema p
5	97	96.0	348	09ALV7	09ALV7 treponema p
6	97	96.0	393	093CA3	093CA3 treponema p
7	97	96.0	428	09ALV6	09ALV6 treponema p
8	97	96.0	328	SWI6_SCHPO	P40381 schizosach
9	52	51.5	533	07QI86	07QI86 anopheles g
10	51	50.5	77	07XMT2	07XMT2 oryza sativ
11	50	49.5	166	09FXB0	09FXB0 arabidopsis
12	50	49.5	749	YU20_HUMAN	09Y319 homo sapien
13	49	48.5	699	08IIO9	08IIO9 plasmodium
14	49	48.5	719	02S826	02S826 plasmodium
15	48	47.5	226	08S2R0	08S2R0 oryza sativ
16	48	47.5	482	092YV8	092YV8 rhizobium m
17	48	47.5	491	092YV6	092YV6 rhizobium m
18	48	47.5	723	07XG22	07XG22 oryza sativ
19	48	47.5	723	094I06	094I06 oryza sativ
20	48	47.5	742	06P9B2	06P9B2 homo sapien
21	48	47.5	742	AAH60851	AAH60851 homo sapi
22	48	47.5	776	09JG99	09JG99 porcine ast
23	48	47.5	122	09JH64	09JH64 porcine ast
24	47	46.5	783	09KXH4	09KXH4 yersinia en
25	47	46.5	165	09YRC4	09YRC4 drosophila
26	47	46.5	187	09S1U8	09S1U8 arabidopsis
27	47	46.5	193	094I15	094I15 arabidopsis
28	47	46.5	286	08QORU5	08QORU5 chimpanzee
29	47	46.5	357	06ZAB0	06ZAB0 oryza sativ
30	47	46.5	379	BAD03360	BAD03360 oryza sat
31	47	46.5	379	Q8MQ44	Q8MQ44 caenorhabdi

32	47	46.5	411	2	Q8MQ45
33	47	46.5	463	1	Q9P3C3
34	47	46.5	471	2	P34437 caenorhabdi
35	47	46.5	541	1	P19527 rattus norv
36	47	46.5	572	2	Q9NVZ8
37	47	46.5	678	2	Q8I1C5
38	47	46.5	752	2	Q86X86
39	47	46.5	944	2	Q8CG11
40	47	46.5	1174	2	Q6ZQ43
41	47	46.5	1174	2	BAC98029
42	47	46.5	1189	2	Q9NYU0
43	47	46.5	1431	2	Q96T23
44	47	46.5	1841	2	Q3J958
45	46	45.5	159	1	R1SB_CORGL

ALIGNMENTS

RESULT 1	PRELIMINARY	PRT	256 AA.
083448			
AC	083448		
DT	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	Hypothetical protein TP0433.		
GN	OrderedAccessNames=TP0433;		
OC	Treponema pallidum.		
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.		
OX	NCBI_Taxid=160;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Nichols		
RX	MEDLINE=98332770; PubMed=9665876;		
RA	Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G., Dodson R.J., Gwin M.L., Hickey E.K., Clayton R.A., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D., Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M., Utterback T.R., McDonald L.A., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M., Weidman J.F., Smith H.O., Venter J.C.;		
RT	"Complete genome sequence of Treponema pallidum, the syphilis agent"		
RL	GenBank:281375-388(1998).		
DR	EMBL: AB001220; AAC65421.1; -		
DR	PIR: F71326; F71326.		
DR	TIGR: TP0433; -		
KM	Complete proteome; Hypothetical protein.		
SO	SEQUENCE 256 AA; 27453 MW; E90329D25A119E76 CRC64;		
Query Match	100.0%; Score 101; DB 2; Length 256;		
Best Local Similarity	100.0%; Pred. No. 5.9e-07;		
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 PKVPEPASERGEGEREVEDA 20		
Db	189 PKVPEPASERGEGEREVEDA 208		
RESULT 2	PRELIMINARY;	PRT;	432 AA.
ID	051953		
AC	051953		
DT	01-JUN-1998 (TREMBLrel. 06, Created)		
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)		
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)		
DE	Acidic repeat protein.		
OS	Treponema pallidum.		
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.		
OX	NCBI_Taxid=160;		
RN	[1]		
RP	SEQUENCE FROM N.A.		

Complete Genome

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 18.9507 Seconds
(without alignment)
378.592 Million cell updates/sec

Title: US-10-017-168-9

Perfect score: 101
Sequence: 1 PKYVEPASEREGGERVEDA 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	20	AAB48321	Aab48321 T. pallid
2	101	100.0	432	AAB48316	Aab48316 T. pallid
3	97	96.0	232	AAB48317	Aab48317 T. pallid
4	97	96.0	312	AAB48318	Aab48318 T. pallid
5	85	84.2	21	AAB48325	Aab48325 T. pallid
6	77	76.2	20	AAB48329	Aab48329 T. pallid
7	77	76.2	20	AAB48328	Aab48328 T. pallid
8	77	76.2	20	AAB48327	Aab48327 T. pallid
9	67	66.3	20	AAB48320	Aab48320 T. pallid
10	62	61.4	26	AAB48326	Aab48326 T. pallid
11	58	57.4	20	AAB48330	Aab48330 T. pallid
12	51	50.5	296	ABG15624	Novel hum
13	50	49.5	133	ABG21773	Arabidops
14	50	49.5	163	ADP83534	Human GRI
15	50	49.5	166	AAG21772	Arabidops
16	50	49.5	166	ADN74723	Thale cre
17	50	49.5	749	AAW78419	Human pro
18	50	49.5	749	AAW78419	Human pro
19	50	49.5	749	ADP83530	Human GRI
20	50	49.5	749	ADP69653	Human hea
21	50	49.5	754	AAW20997	Human nuc
22	50	49.5	757	AAW79403	Human pro
23	50	49.5	790	AAW41603	Human ORF
24	48	47.5	888	ABP73624	Abp73624 Candida a
25	47	46.5	69	AAU41010	AAU41010 Propionib

26	47	46.5	69	6	ABM37529	Abm37529 Propionib
27	47	46.5	79	3	AAG61691	Aag61691 Arabidops
28	47	46.5	95	4	AAO04657	Aao04657 Human pol
29	47	46.5	165	4	ABB65571	Abb65571 Drosophil
30	47	46.5	187	3	AAG16629	Aag16629 Arabidops
31	47	46.5	187	3	AAG50350	Aag50350 Arabidops
32	47	46.5	386	4	ABR83349	AbR83349 Partial s
33	47	46.5	386	4	AAW67331	AAW67331 Amino aci
34	47	46.5	432	4	AAU16231	AAU16231 Human nov
35	47	46.5	432	6	ABU55300	AbU55300 Human nov
36	47	46.5	509	7	AD160459	Ad160459 Secreted
37	47	46.5	541	7	ADE57652	AdE57652 Rat Prote
38	47	46.5	542	6	ABM04812	Abm04812 Rat NF-L.
39	47	46.5	572	4	AAW92788	AAW92788 Human pro
40	47	46.5	583	4	AAW25397	AAW25397 Human pro
41	47	46.5	719	3	AAW42618	AAW42618 Human ORF
42	47	46.5	942	4	ABG10600	Abg10600 Novel hum
43	47	46.5	1398	5	ABG97491	AbG97491 Human NOV
44	47	46.5	1400	4	ABR83348	AbR83348 AAP-2 pro
45	47	46.5	1445	6	ABR41365	AbR41365 Human DIT

ALIGNMENTS

RESULT 1
ID AAB48321 standard; peptide; 20 AA.
XX
AC AAB48321;
XX
DT 20-APR-2001 (first entry)
XX
DE T. pallidum acidic repeat protein immunogenic peptide arp 3.
XX
KM Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
XX yaws; bejel.
OS Treponema pallidum.
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016425.
XX
PR 14-JUN-1999; 99US-0138981P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;
XX
WP1; 2001-080711/09.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample.
PS Claim 15; Fig 11; 73pp; English.
XX
XX The invention relates to a method of detecting presence of Treponema
XX pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
XX sample that involves contacting an acidic repeat protein (arp), or one or
XX more isolated immunogenic TP peptides of arp with an Ab containing
XX biological sample and then detecting the formation of a complex between
XX immunogenic peptides and Ab. The presence of the complex indicates the
XX presence of TP. The method is thus useful for diagnosing syphilis, yaws,
XX and bejel diseases. The immunogenic peptides or the Abs raised against
XX arp, as part of an immunogenic composition, are useful for inducing a
XX protective immune response against syphilis, yaws or bejel caused by TP.
XX Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
XX arp protein

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 ; Search time 21.936 seconds

(without alignments)
655.635 Million cell updates/sec

Title: US-10-017-168-11

Perfect score: 124
Sequence: 1 GHAGIPGLVSLAPAAAGLGIGVY 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	124	100.0	256	2	083448
2	124	100.0	348	2	09ALV7
3	124	100.0	393	2	093CA3
4	124	100.0	428	2	09ALV6
5	124	100.0	432	2	051953
6	124	100.0	548	2	093CA4
7	63	50.8	458	2	073NG7
8	63	50.8	458	2	AA511704
9	57.5	46.4	362	2	089FH6
10	56.5	45.6	666	2	028096
11	56.5	45.6	679	2	028097
12	56.5	45.6	707	2	028098
13	56.5	45.6	747	1	EL5_BOVIN
14	55	44.4	272	2	09ASV6
15	55	44.4	387	2	07V125
16	55	44.4	387	2	07VBF7
17	54	43.5	294	2	08W008
18	53.5	43.1	242	1	YK81_STRCO
19	53.5	43.1	342	2	09XAN5
20	53	42.7	249	2	089LRO
21	53	42.7	319	1	RNZ_SYNPX
22	53	42.7	675	2	07G5W5
23	52.5	42.3	810	2	09ESZ9
24	52.5	42.3	860	1	EL5_MOUSE
25	52.5	42.3	860	2	08C5L8
26	52	41.9	650	2	028099
27	51	41.1	266	2	074F10
28	51	41.1	266	2	AAR34129
29	51	41.1	426	2	06D7J1
30	51	41.1	430	2	09L0U3
31	51	41.1	453	2	07NWT7

ALIGNMENTS

32	51	41.1	557	2	089FZ3	089fz3 bradyrhizob
33	51	41.1	580	2	08VQZ5	08vqz5 myxococcus
34	50.5	40.7	182	2	08C8W0	08c8w0 mus musculu
35	50.5	40.7	593	2	044099	044099 anaplasma m
36	50.5	40.7	622	2	09APG5	09apg5 anaplasma m
37	50.5	40.7	623	2	09APG6	09apg6 anaplasma m
38	50.5	40.7	623	2	09APG7	09apg7 anaplasma m
39	50.5	40.7	623	2	093M65	093m65 anaplasma m
40	50.5	40.7	624	2	06V0Y4	06v0y4 anaplasma m
41	50.5	40.7	624	2	AA055853	AA055853 anaplasma
42	50.5	40.7	651	2	07MTV8	07mtv8 anaplasma m
43	50.5	40.7	652	2	044100	044100 anaplasma m
44	50.5	40.7	680	2	06RVB1	06rvb1 anaplasma m
45	50.5	40.7	680	2	AAR33046	AAR33046 anaplasma

RESULT 1

ID	083448	PRELIMINARY;	PRT;	256 AA.
AC	083448			
DT	01-NOV-1998	(TREMBLrel. 08, Created)		
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)		
DE	Hypothetical protein TP0433.			
GN	OrderedLocustNames=TP0433;			
OS	Treponema pallidum.			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
NCBI_TaxID=160;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Nichols.			
RX	MEDLINE=98332770; PubMed=9665876;			
RA	Frazer C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,			
RA	Dodson R.J., Gwin M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,			
RA	Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,			
RA	Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,			
RA	Uteerback T.R., McDonald L.A., Artlich P., Bowman C., Cotton M.D.,			
RA	Fuji C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,			
RA	Weidman J.F., Smith H.O., Venter J.C.;			
RT	"Complete genome sequence of Treponema pallidum, the syphilis			
RT	spirochete.";			
RL	Science 281:375-388(1998).			
DR	EMBL; AB001220; AAC65421.1; -			
DR	PIR; F71326; F71326.			
DR	TIGR; TP0433; -			
KW	Complete proteome; Hypothetical protein.			
SEQ	SEQUENCE 256 AA; 27453 MW; E90329D25A119E76 CRC64;			
Query Match 100.0%; Score 124; DB 2; Length 256;				
Best Local Similarity 100.0%; Pred. No. 1,99-08;				
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 GHAGIPGLVSLAPAAAGLGIGVY 25			
DB	87 GHAGIPGLVSLAPAAAGLGIGVY 111			
RESULT 2				
ID	09ALV7	PRELIMINARY;	PRT;	348 AA.
AC	09ALV7			
DT	01-JUN-2001	(TREMBLrel. 17, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-OCT-2002	(TREMBLrel. 22, Last annotation update)		
DE	Acidic repeat protein.			
GN	Name=arp;			
OS	Treponema pallidum (subsp. pertenue) (Yaws treponeme).			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
NCBI_TaxID=168;				
RN	[1]			

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24 ; Search time 3.89507 Seconds
(without alignments)
617.555 Million cell updates/sec

Title: US-10-017-168-11

Perfect score: 124
Sequence: 1 GHAGIPGLVSLAPAAAQIGIGVY 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	124	100.0	256 2 F71326	hypothetical prote
2	56.5	45.6	747 1 EABO	elastin precursor,
3	55	44.4	272 2 F87351	hypothetical prote
4	53.5	43.1	242 2 T34851	hypothetical prote
5	53.5	43.1	347 2 T35013	probable membrane
6	53	42.7	770 2 S59623	tropoelastin - she
7	52.5	42.3	860 1 EAMS	elastin precursor
8	50.5	40.7	767 2 A35645	major surface prot
9	50	40.3	668 2 F83287	hypothetical prote
10	50	40.3	792 1 EAHU	elastin precursor,
11	49.5	39.9	377 2 F95948	probable acyltrans
12	49.5	39.9	434 2 S04534	invasin precursor
13	49	39.5	105 2 C97828	hypothetical prote
14	49	39.5	349 2 T44856	myoglobin transpo
15	49	39.5	400 2 H83536	hypothetical prote
16	49	39.5	459 2 UC7931	cellulohydrolyase
17	49	39.5	603 2 S34130	serine/chreonine-s
18	49	39.5	1053 2 B70987	probable PPE prote
19	48.5	39.1	320 2 F82763	D-alanine-D-alanin
20	48.5	39.1	542 2 AE3057	phosphoglucomutase
21	48.5	39.1	567 2 A96829	phosphoglucomutase
22	48.5	39.1	864 1 EAPR	elastin precursor
23	48	38.7	181 2 F83907	hypothetical prote
24	48	38.7	195 2 S32123	glycine-rich prote
25	48	38.7	202 2 B87342	hypothetical prote
26	48	38.7	334 2 F86462	AIg1-like protein,
27	48	38.7	333 2 T34631	probable integrin
28	48	38.7	421 2 A26691	cell cycle regulat
29	48	38.7	522 2 T31310	hypothetical prote

30	48	38.7	784 2 A26601	elastin precursor
31	47.5	38.3	441 2 H82642	hypothetical prote
32	47	37.9	290 2 B87679	integral membrane
33	47	37.9	296 2 I40328	serum-resistance p
34	47	37.9	387 2 T44873	probable secreted
35	47	37.9	464 2 A81480	PTS system, fructo
36	47	37.9	464 2 AG1119	PTS system, fructo
37	47	37.9	614 2 D87410	fold protein [limp
38	47	37.9	619 2 A13336	potassium/proton a
39	46.5	37.5	245 2 T03534	precortin-3 methyl
40	46.5	37.5	355 2 H80245	conserved hypothec
41	46.5	37.5	399 2 A55577	formaldehyde dehyd
42	46.5	37.5	476 2 F83286	probable glycosyla
43	46.5	37.5	511 2 D97965	hypothetical prote
44	46.5	37.5	511 2 H95097	sugar ABC transpor
45	46.5	37.5	566 2 AH3487	phosphoglucomutase

ALIGNMENTS

RESULT 1
F71326
hypothetical protein TP0433 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: F71326
R/Frazer, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.;
rean, J.; Khaliq, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uettersack, T.;
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: AV7250; MUID:98332770; PMID:9665876
A/Accession: F71326
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-256 <COL>
A/Cross-references: UNIPROT:O83448; GB:AEO01220; GB:AEO30520; NID:g3322705; PIDN:AA
A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0433

Query Match 100.0%; Score 124; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHAGIPGLVSLAPAAAQIGIGVY 25
DB 87 GHAGIPGLVSLAPAAAQIGIGVY 111

RESULT 2
EABO
elastin precursor, splice form a - bovine
N/Alternate names: tropoelastin
N/Contains: elastin precursor, splice form b; elastin precursor, splice form c
C/Species: Bos primigenius taurus (cattle)
C/Date: 08-Jun-1989 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: A11865; A26728; B26728; C26728; A22343; I15886
R/Rien, H.; Anderson, N.; Ornstein-Goldstein, N.; Baehlt, M.M.; Rosenbloom, J.C.; Ab
Biochemistry 28, 2365-2370, 1989
A/Title: Structure of the bovine elastin gene and SI nuclease analysis of alternati
A/Reference number: A11865; MUID:89274159; PMID:2543440
A/Accession: A11865
A/Molecule type: DNA
A/Residues: 1-27 <YEH>
A/Cross-references: UNIPROT:P04985; UNIPROT:Q28101; GB:J02855; NID:G340504; PIDN:AA
J.Raju, K.; Anwar, R.A.
J. Biol. Chem. 262, 5755-5762, 1987
A/Title: Primary structures of bovine elastin a, b, and c deduced from the sequence
A/Reference number: A92640; MUID:87194772; PMID:3032943
A/Accession: A26728
A/Molecule type: mRNA

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OM protein - protein search, using ew model

Run on: January 28, 2005, 10:59:24 ; Search time 23.6884 Seconds
(without alignments) 378.592 Million cell updates/sec

Title: US-10-017-168-11

Sequence: 1 GHAGIPGLIVSLAPAAAOLGICVY 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	124	100.0	25	AA848323	Aab48323 T. pallid
2	124	100.0	232	AA848317	Aab48317 T. pallid
3	124	100.0	312	AA848318	Aab48318 T. pallid
4	124	100.0	432	AA848316	Aab48316 T. pallid
5	60	48.4	1257	ABO68544	ABO68544 Pseudomon
6	59.5	48.0	843	ABO80824	ABO80824 Novel pro
7	54.5	44.0	1133	ABO83385	ABO83385 Pseudomon
8	51	44.1	28	AA815028	AA815028 Part of e
9	51	44.1	283	AA812779	AA812779 Arabidops
10	51	44.1	306	AA812778	AA812778 Arabidops
11	51	44.1	340	AA812777	AA812777 Arabidops
12	51	44.1	352	ABO66983	ABO66983 Klebsiell
13	51	44.1	437	ABO74993	ABO74993 Pseudomon
14	50.5	40.7	593	AA808404	AA808404 Amv105 en
15	50.5	40.7	652	AA808403	AA808403 Amv105 en
16	50.5	40.7	767	AA807599	AA807599 Sequence
17	50.5	40.7	767	AA808401	AA808401 Amv105 en
18	50	40.3	147	AA801304	AA801304 Human tro
19	50	40.3	171	AA869137	AA869137 Amino aci
20	50	40.3	183	AA801311	AA801311 Human tro
21	50	40.3	183	AA869138	AA869138 Amino aci
22	50	40.3	200	AA801305	AA801305 Human tro
23	50	40.3	216	AA801310	AA801310 Human tro
24	50	40.3	421	ABO70994	ABO70994 Pseudomon
25	50	40.3	472	AA888422	AA888422 Human mem

26	50	40.3	617	7	ADB64761	ADB64761 Human pro
27	50	40.3	630	7	ABO71076	ABO71076 Pseudomon
28	50	40.3	660	2	AA801303	AA801303 Human tro
29	50	40.3	663	7	ADM03792	ADM03792 Human tro
30	50	40.3	692	7	ADB40134	ADB40134 Human pro
31	50	40.3	698	2	AA801302	AA801302 Human tro
32	50	40.3	698	2	AA869069	AA869069 Amino aci
33	50	40.3	711	7	ADB40132	ADB40132 Human tro
34	50	40.3	712	3	AA808630	AA808630 Human NOV
35	50	40.3	730	2	AAW46315	AAW46315 Amino aci
36	50	40.3	730	3	AA808631	AA808631 Human eia
37	50	40.3	730	5	AA8017360	AA8017360 Fusion pr
38	50	40.3	730	8	ADQ19747	ADQ19747 Human eia
39	50	40.3	731	3	AA869068	AA869068 Human eia
40	50	40.3	731	4	AA866657	AA866657 Amino aci
41	50	40.3	731	6	ABU08725	ABU08725 Human eia
42	50	40.3	731	7	ADL96420	ADL96420 Human eia
43	50	40.3	733	2	AA856653	AA856653 Synthetic
44	50	40.3	733	2	AA801301	AA801301 Amino aci
45	50	40.3	757	7	ABG75223	ABG75223 Human tro

ALIGNMENTS

RESULT 1
AAB48323
ID AAB48323 standard; peptide; 25 AA.
XX
AC AAB48323;
XX
DT 20-APR-2001 (first entry)
XX
DE T. pallidum acidic repeat protein immunogenic peptide arp 5.
XX
KM Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
XX
KW yaws; bejel.
XX
OS Treponema pallidum.
XX
PN WO20007746-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016425.
XX
PR 14-JUN-1999; 99US-0138981P.
XX
(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
Liu H, Steiner B, Rhodes B;
XX
WPI, 2001-080711/09.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample.
XX
PS Claim 15; Fig 11; 73pp; English.
XX
The invention relates to a method of detecting presence of Treponema
XX pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
XX sample that involves contacting an acidic repeat protein (arp), or one or
XX more isolated immunogenic TP peptides of arp with an Ab containing
XX biological sample and then detecting the formation of a complex between
XX immunogenic peptides and Ab. The presence of the complex indicates the
XX presence of TP. The method is thus useful for diagnosing syphilis, yaws,
XX and bejel diseases. The immunogenic peptides or the Abs raised against
XX arp, as part of an immunogenic composition, are useful for inducing a
XX protective immune response against syphilis, yaws or bejel caused by TP.
XX Sequences AAB48319-AAB8330 represent immunogenic peptides of T. pallidum
XX arp protein

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24 ; Search time 3.89507 Seconds
(without alignments)

617.555 Million cell updates/sec

Title: US-10-017-168-12

Perfect score: 137
Sequence: 1 VPARPQRDPUSPPAGHTVPEYRD 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	137	100.0	256	2 F71326
2	60	43.8	97	2 G70866
3	52	38.0	212	2 C72464
4	52	38.0	622	2 S56214
5	51	37.2	678	2 G75524
6	51	37.2	982	2 S09810
7	51	37.2	1192	2 T17255
8	51	37.2	2140	2 T18543
9	50	36.5	197	2 S57948
10	50	36.5	417	2 T23024
11	50	36.5	827	2 AC2963
12	50	36.5	881	2 B96320
13	50	36.5	1057	2 T04874
14	50	36.5	1102	2 T28666
15	50	36.5	6420	2 T30283
16	49	35.8	173	2 B39141
17	49	35.8	396	1 UH0633
18	49	35.8	718	1 TNBEF6
19	49	35.8	760	2 T06291
20	49	35.8	900	2 B87957
21	49	35.8	948	2 T26417
22	49	35.8	2115	2 S39480
23	49	35.8	2205	1 MNWYRN
24	48	35.0	101	2 D83375
25	48	35.0	132	2 A75491
26	48	35.0	333	2 H87220
27	48	35.0	443	2 A38219
28	48	35.0	499	1 CPBHS
29	48	35.0	510	1 S43516

ALIGNMENTS

RESULT 1

F71326
hypothetical protein TP0433 - syphilis spirochete

C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C/Accession: F71326
R/Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw

rean, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; Mc
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; MUID:96332770; PMID:9665876

A/Accession: F71326
A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-256 <COL>
A/Cross-references: UNIPROT:O83448; GB:AE001220; GB:AE000520; NID:g3322705; PIDN:AA065

A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0433

Query Match 100.0%; Score 137; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VPARPQRDPUSPPAGHTVPEYRD	25
DB	144	VPARPQRDPUSPPAGHTVPEYRD	168

RESULT 2

G70866
hypothetical protein RV2472 - Mycobacterium tuberculosis (strain H37RV)

C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C/Accession: G70866
R/Cole, S.T.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,

Reid, R.; Connor, R.; Brown, R.; Devlin, K.; Felwell, T.; Gentile, S.; Hamlin, N.; Holroyd,
Reid, R.; Connor, R.; Brown, R.; Devlin, K.; Felwell, T.; Gentile, S.; Hamlin, N.; Holroyd,

Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom
A/Reference number: A70500; MUID:96295987; PMID:9634230

A/Accession: G70866
A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-97 <COL>
A/Cross-references: UNIPROT:O53199; GB:AL021246; GB:AL123456; NID:g33261507; PIDN:CAA16

A/Experimental source: strain H37RV
C/Genetics:
A/Gene: RV2472

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 23.6884 Seconds
(without alignments)
378.592 Million cell updates/sec

Title: US-10-017-168-12

Perfect score: 137
Sequence: 1 VPARPAPDRPLSPSPAPHTYPEYRD 25

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseq_23Sep04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	100.0	25	AA848324	Aab48324 T. pallid
2	137	100.0	232	AA848317	Aab48317 T. pallid
3	137	100.0	312	AA848318	Aab48318 T. pallid
4	137	100.0	432	AA848316	Aab48316 T. pallid
5	59.5	43.4	325	ABO77834	AbO77834 Pseudomon
6	57.5	42.0	476	ABG03460	Abg03460 Novel hum
7	57.5	42.0	476	ABO00838	AbO00838 Polypepti
8	57.5	41.6	126	AA821113	Aam82113 Human hae
9	57	41.6	322	AA840075	Aam40075 Human pol
10	57	41.6	362	ABG03440	Abg03440 Novel hum
11	57	41.6	387	ABG27023	Abg27023 Novel hum
12	57	41.6	491	AA82316	Aaw62316 Mouse pro
13	57	41.6	647	AD867649	Ad867649 Ly1484 Bn
14	57	41.6	647	AD867647	Ad867647 Human Ly4
15	57	41.6	989	ABU21195	Abu21195 Protein e
16	57	41.6	1270	ABU19769	Abj19769 Human MP2
17	57	41.6	1270	AD867643	Ad867643 Human Ly4
18	57	41.6	1270	AD867648	Ad867648 Ly1484 Jo
19	57	41.6	1338	AD840104	Ad840104 Human NOV
20	56	40.9	147	AA002546	Aa002546 Human pol
21	56	40.9	444	AAU52218	Aau52218 Propionib
22	56	40.9	444	ABM48737	Abm48737 Propionib
23	55.5	40.5	614	ABO71464	AbO71464 Pseudomon
24	55.5	40.5	2768	AB868397	Ab868397 Drosophil
25	55	40.1	455	AA843987	Aab43987 Human can

26	54	39.4	43	4	ABG27642	ABg27642 Novel hum
27	54	39.4	104	7	ADB74290	ADB74290 Mycobacte
28	54	39.4	232	3	AA509923	AAy509923 Human fet
29	54	39.4	771	4	ABG29770	ABg29770 Novel hum
30	54	39.4	771	4	ABG08952	ABg08952 Novel hum
31	53	38.7	95	4	AAU68811	Aau68811 Novel hum
32	53	38.7	95	7	AD860145	Ad860145 Connectiv
33	53	38.7	356	7	ABO71186	AbO71186 Pseudomon
34	53	38.7	383	7	ABO78341	AbO78341 Pseudomon
35	53	38.7	654	6	ABU19399	AbU19399 Human int
36	52.5	38.3	157	7	ABO72101	AbO72101 Pseudomon
37	52.5	38.3	469	7	ABO83858	AbO83858 Pseudomon
38	52.5	38.3	1169	4	ABG14729	ABg14729 Novel hum
39	52.5	38.3	1294	4	AA840906	Aam40906 Human pol
40	52	38.0	306	4	AAU62236	Aau62236 Propionib
41	52	38.0	306	6	ABM58755	Abm58755 Propionib
42	52	38.0	312	8	ADG22417	Adg22417 Cyanophag
43	52	38.0	622	6	ABR53818	AbR53818 Protein s
44	52	38.0	622	7	ADK65006	Adk65006 Disease t
45	52	38.0	625	8	AD145445	Ad145445 Rice isop

ALIGNMENTS

RESULT 1
ID AAB48324 standard; peptide; 25 AA.
XX AAB48324;
XX
XX 20-APR-2001 (first entry)
XX
XX
DE T. pallidum acidic repeat protein immunogenic peptide arp 6.
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW yaws; bejel.
XX
OS Treponema pallidum.
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016425.
XX
PR 14-JUN-1999; 99US-0138981P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Liu H, Steiner B, Rhodes B;
XX WPI; 2001-080711/09.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample.
XX
PS Claim 15; Fig 11; 73pp; English.
XX
XX The invention relates to a method of detecting presence of Treponema
XX pallidum (TP), anti-Treponema antibodies (Abs), or both in a biological
XX sample that involves contacting an acidic repeat protein (arp), or one or
XX more isolated immunogenic TP peptides of arp with an Ab containing
XX immunogenic peptides and then detecting the formation of a complex between
XX presence of TP. The method is thus useful for diagnosing syphilis, yaws,
XX and bejel diseases. The immunogenic peptides or the Abs raised against
XX arp, as part of an immunogenic composition, are useful for inducing a
XX protective immune response against syphilis, yaws or bejel caused by TP.
XX Sequences AAB8319-AAB8330 represent immunogenic peptides of T. pallidum
XX arp protein

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 ; Search time 18.4293 Seconds
(without alignments)
655.635 Million cell updates/sec

Title: US-10-017-168-13

Perfect score: 105
Sequence: 1 VVEPASERGEREVEDVPKV 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_02 :
1: uniprot_sprot :
2: uniprot_trembl :*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	105	100.0	256 2	083448
2	105	100.0	348 2	09ALV7
3	105	100.0	393 2	093CA3
4	105	100.0	428 2	09ALV6
5	105	100.0	432 2	051953
6	105	100.0	548 2	093CA4
7	98	93.3	227 2	083449
8	56	53.3	533 2	07Q186
9	55	52.4	3038 1	TRIO HUMAN
10	53	50.5	449 2	09LS16
11	52	49.5	543 2	094434
12	52	49.5	558 2	095Y77
13	51	48.6	362 2	06UE13
14	51	48.6	362 2	AAT12523
15	51	48.6	1372 2	09VNA6
16	51	48.6	1372 2	08SX99
17	50	47.6	183 2	06N585
18	50	47.6	183 2	CAE28537
19	50	47.6	474 2	097Y15
20	50	47.6	585 2	09F3N0
21	50	47.6	699 2	081109
22	50	47.6	719 2	025826
23	49	46.7	471 2	081ZP7
24	49	46.7	1135 2	07MWB2
25	48.5	46.2	328 1	SW16_SCHPO
26	48	45.7	154 2	039814
27	48	45.7	226 2	08S2R0
28	48	45.7	650 2	06DDE9
29	48	45.7	652 2	08TWM1
30	48	45.7	723 2	07XG22
31	48	45.7	723 2	094106

32	48	45.7	2999 2	08CH17	08ch17 mus musculu
33	48	45.7	3035 2	08CH18	08ch18 mus musculu
34	47.5	45.2	379 2	09GL13	09gl13 macropus ru
35	47	44.8	165 2	09VRC4	09vrc4 drosophila
36	47	44.8	220 2	08P420	08p420 xanthomonas
37	47	44.8	221 2	09K959	09k959 bacillus ha
38	47	44.8	373 2	06H188	06h188 issatchenki
39	47	44.8	508 2	045345	045345 caenorhabdi
40	47	44.8	517 1	GUAA_LACRH	085192 lactobacilli
41	47	44.8	541 1	NFL_RAT	p19527 rattus norv
42	47	44.8	616 2	08ECM5	08ecm5 shewanella
43	47	44.8	905 2	09UVAO	09uvao issatchenki
44	47	44.8	1174 2	06Z043	06z043 mus musculu
45	47	44.8	1174 2	BAC98029	Bac98029 mus muscu

ALIGNMENTS

RESULT 1

ID	083448	PRELIMINARY:	PRT:	256 AA.
AC	083448:			
DT	01-NOV-1998 (TREMBlrel. 08, Created)			
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)			
DT	01-JUN-2003 (TREMBlrel. 24, Last annotation update)			
DE	Hypothetical protein TP0433.			
GN	OrderedLocustNames=TP0433;			
OS	Treponema pallidum.			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=160;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Nichols.			
RX	MEDLINE=98332770; PubMed=9665876;			
RA	Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,			
RA	Dodson R.J., Gwinn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,			
RA	Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,			
RA	Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,			
RA	Usterback T.R., McDonald L.A., Artlach P., Bowman C., Cotton M.D.,			
RA	Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,			
RA	Weidman J.F., Smith H.O., Venter J.C.;			
RT	"Complete genome sequence of Treponema pallidum, the syphilis			
RT	spirochete."			
RL	Science 281:375-388(1998).			
DR	EMBL; AE001220; AAC55421.1; -.			
DR	PIR; F71326; F71326.			
DR	TIGR; TP0433; -.			
KW	Complete proteome; Hypothetical protein.			
SQ	SEQUENCE 256 AA; 27453 MW; E90329D25A119E76 CRC64;			
Query Match				
Best Local Similarity 100.0%; Score 105; DB 2; Length 256;				
Matches 21; Conservative 100.0%; Pred. No. 1.3e-07;				
Mismatches 0; Indels 0; Gaps 0;				
Oy	1	VVEPASERGEREVEDVPKV 21		
Db	231	VVEPASERGEREVEDVPKV 251		
RESULT 2				
09ALV7		PRELIMINARY:	PRT:	348 AA.
ID	09ALV7:			
AC	09ALV7:			
DT	01-JUN-2001 (TREMBlrel. 17, Created)			
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)			
DT	01-OCT-2002 (TREMBlrel. 22, Last annotation update)			
DE	Acidic repeat protein.			
GN	Name=arp;			
OS	Treponema pallidum (subsp. pertenue) (Yaws treponeme).			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=160;			
RN	[1]			

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 19.8963 Seconds
(without alignments)
378.592 Million cell updates/sec

Title: US-10-017-168-13

Perfect score: 105

Sequence: 1 VVEPASREGEREVEDVPKV 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23sep04:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003as:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	21	AA848325	Aab48325 T. pallid
2	105	100.0	232	AA848317	Aab48317 T. pallid
3	105	100.0	312	AA848318	Aab48318 T. pallid
4	105	100.0	432	AA848316	Aab48316 T. pallid
5	85	81.0	20	AA848321	Aab48321 T. pallid
6	65	61.9	20	AA848329	Aab48329 T. pallid
7	65	61.9	20	AA848328	Aab48328 T. pallid
8	65	61.9	20	AA848327	Aab48327 T. pallid
9	62	59.0	26	AA848326	Aab48326 T. pallid
10	55	52.4	20	AA848320	Aab48320 T. pallid
11	55	52.4	2980	ABG20756	Abg20756 Novel hum
12	55	52.4	3038	ABG17025	Abg17025 Novel hum
13	55	52.4	3038	ABM32684	Abm32684 Human Tr1
14	55	52.4	3038	ABO07226	AbO07226 Human p53
15	55	52.4	3060	ABG06311	AbG06311 Novel hum
16	53	50.5	20	AA848330	Aab48330 T. pallid
17	53	50.5	449	ABR93640	Abp93640 Hericida
18	51	48.6	1167	ABR57757	Abb57757 Drosophi
19	49	46.7	121	ADR60314	Adt60314 Human con
20	49	46.7	216	ADP58964	AdP58964 Human pol
21	49	46.7	471	AAO26610	Aao26610 Human 6-O
22	49	46.7	472	ADH72050	Adh72050 Human pro
23	49	46.7	472	ADH72052	Adh72052 Human pro
24	49	46.7	472	ADH72038	Adh72038 Human pro
25	49	46.7	944	AD116666	Ad116666 Human NOV

26	49	46.7	944	8	ADN42320	Adn42320 Human nov
27	48	45.7	154	2	AA228301	Aa228301 Amino aci
28	48	45.7	652	7	ADM26621	Adm26621 Hyperther
29	47.5	45.2	296	4	ABG15624	Abg15624 Novel hum
30	47	44.8	165	4	ABR65571	AbR65571 Drosophi
31	47	44.8	541	7	ADE57652	AdE57652 Rat Prote
32	47	44.8	542	6	ABM04812	AbM04812 Rat NF-L
33	47	44.8	3353	5	AAU82706	Aau82706 Amino aci
34	46	43.8	33	2	AA872825	Aa872825 Mitocobn r
35	46	43.8	159	4	AA879915	Aa879915 Coryneb
36	46	43.8	159	4	AA879916	Aa879916 Coryneb
37	46	43.8	159	4	AA879917	Aa879917 Coryneb
38	46	43.8	163	7	ADP83534	AdP83534 Human GRI
39	46	43.8	187	8	ADM57223	AdM57223 A thalian
40	46	43.8	305	7	ADN95157	Adn95157 Human BEC
41	46	43.8	306	8	ADO24505	Ado24505 Human PRO
42	46	43.8	409	5	AAO17170	Aao17170 Human sec
43	46	43.8	409	5	AAE21624	Aae21624 Human gen
44	46	43.8	409	5	ABG64754	AbG64754 Human alb
45	46	43.8	409	7	ADN95109	Adn95109 Human LEC

ALIGNMENTS

RESULT 1	AA848325	standard; peptide: 21 AA.
ID	AA848325	
AC	AA848325;	
DT	20-APR-2001	(first entry)
XX	T. pallidum acidic repeat protein immunogenic peptide arp 7.	
DE	T. pallidum acidic repeat protein immunogenic peptide arp 7.	
XX	Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;	
KW	yaws; bejel.	
XX	Treponema pallidum.	
OS	WO200077486-A2.	
XX	21-DEC-2000.	
PD	14-JUN-2000; 2000WO-US016425.	
PF	14-JUN-1999; 99US-0138981P.	
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
PA	Liu H, Steiner B, Rhodes B;	
XX	WPI; 2001-080711/09.	
DR	Detecting Treponema pallidum in blood, saliva, etc., by detecting	
XX	formation of a complex between immunogenic peptides of acidic repeat	
PT	protein of the bacterium and an antibody present in the biological	
PT	sample.	
XX	Claim 15, Fig 11; 73pp; English.	
PS	The invention relates to a method of detecting presence of Treponema	
CC	pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological	
CC	sample that involves contacting an acidic repeat protein (arp), or one or	
CC	more isolated immunogenic TP peptides of arp with an Ab containing	
CC	immunogenic peptide and then detecting the formation of a complex between	
CC	presence of TP. The method is thus useful for diagnosing syphilis, yaws,	
CC	and bejel diseases. The immunogenic peptides or the Abs raised against	
CC	arp, as part of an immunogenic composition, are useful for inducing a	
CC	protective immune response against syphilis, yaws or bejel caused by TP.	
CC	Sequences AA848319-AA848330 represent immunogenic peptides of T. pallidum	
CC	arp protein	

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24 ; Search time 4.05087 Seconds
(without alignments)
617.555 Million cell updates/sec

Title: US-10-017-168-14

Perfect score: 137
Sequence: 1 VVEPAGHGEGEREVASQHTKOPSHS 26

Scoring table: BL0SUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	100.0	227	2 G71326	hypothetical prote
2	62	45.3	256	2 F71326	hypothetical prote
3	52	38.0	303	2 B83367	probable glycosyl
4	52	38.0	556	2 T03114	tegument protein -
5	49.5	36.1	2722	2 T20532	hypothetical prote
6	49.5	36.1	2738	2 E88320	protein F07A11.6 l
7	49	35.8	551	2 H69371	probable acid-CoA
8	49	35.8	555	2 D71298	probable uridine k
9	49	35.8	2649	2 T51023	hypothetical prote
10	48	35.0	546	1 S71008	propionyl-CoA carb
11	48	35.0	723	2 AG0887	conserved hypocher
12	47	34.3	445	2 S73703	hypothetical prote
13	47	34.3	467	2 F86468	protein F12K21.24
14	47	34.3	1154	2 S69206	regulator protein
15	47	34.3	1236	2 T50904	Mg protoporphyrin
16	46.5	33.9	161	2 AF0536	conserved hypocher
17	46.5	33.9	519	2 S54300	transketolase (EC
18	46.5	33.9	695	2 S62400	amphiphysin (clone
19	46	33.6	510	2 G96022	probable propionyl
20	46	33.6	510	2 B87494	propionyl-CoA carb
21	46	33.6	707	2 A48686	probable RNA helic
22	46	33.6	1034	2 A36108	integrin alpha-V c
23	45.5	33.2	277	2 T49543	hypothetical prote
24	45.5	33.2	813	2 T12506	hypothetical prote
25	45.5	33.2	1280	2 T00365	hypothetical prote
26	45	32.8	184	2 AF0298	probable yfABCD 1
27	45	32.8	330	2 A82538	pseudouridylylate sy
28	45	32.8	343	2 A86241	hypothetical prote
29	45	32.8	385	1 I39498	GTP cyclohydrolyase

30	45	32.8	413	2 B65088	hypothetical prote
31	45	32.8	424	2 E86367	protein F26F24.22
32	45	32.8	430	2 C23351	serendipity (ary)
33	45	32.8	525	2 A99953	hypothetical prote
34	45	32.8	689	2 S39531	exonuclease ABC c
35	45	32.8	735	2 S54147	alpha adducin - ra
36	45	32.8	739	2 D91116	hypothetical prote
37	45	32.8	739	2 D85961	hypothetical prote
38	45	32.8	1200	2 T48194	hypothetical prote
39	45	32.8	1785	2 T21558	hypothetical prote
40	45	32.8	1929	2 T21559	hypothetical prote
41	44.5	32.5	384	2 A46403	transcription fact
42	44.5	32.5	625	2 A34615	profilaggrin
43	44.5	32.5	650	2 T46660	sulfur controller
44	44	32.1	134	2 H75316	conserved hypocher
45	44	32.1	328	2 A11940	hypothetical prote

ALIGNMENTS

RESULT 1
G71326
hypothetical protein TP0434 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: G71326
R/Fasser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; GwJ
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McI
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; PMID:98332770; PMID:9665876
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-227 <COL>
A/Cross-references: UNIPROT:O83449; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AAC654
A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0434

Query Match 100.0%; Score 137; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVEPAGHGEGEREVASQHTKOPSHS 26
Db 74 VVEPAGHGEGEREVASQHTKOPSHS 99

RESULT 2
F71326
hypothetical protein TP0433 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: F71326
R/Fasser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; GwJ
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McI
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; PMID:98332770; PMID:9665876
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-256 <COL>
A/Cross-references: UNIPROT:O83448; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AAC654
A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0433

Query Match 45.3%; Score 62; DB 2; Length 256;

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 18.9507 Seconds
(without alignments)
378.592 Million cell updates/sec

Title: US-10-017-168-15

Perfect score: 101

Sequence: 1 EVEDPKVPEPASEEGGER 20

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	20	4	AA848327 T. pallid
2	101	100.0	232	4	AA848317 T. pallid
3	101	100.0	312	4	AA848318 T. pallid
4	101	100.0	432	4	AA848316 T. pallid
5	97	96.0	20	4	AA848329 T. pallid
6	96	95.0	20	4	AA848328 T. pallid
7	87	86.1	20	4	AA848320 T. pallid
8	82	81.2	20	4	AA848330 T. pallid
9	77	76.2	20	4	AA848321 T. pallid
10	65	64.4	21	4	AA848325 T. pallid
11	60	59.4	19	4	AA848319 T. pallid
12	53	52.5	26	4	AA848326 T. pallid
13	50	49.5	79	3	AA61691 Arabidops
14	50	49.5	187	3	AA616629 Arabidops
15	50	49.5	187	3	AA650350 Arabidops
16	49	48.5	170	6	ADA55215 Human pro
17	49	48.5	266	4	AA880279 Human pro
18	49	48.5	266	4	AA864379 Human pro
19	49	48.5	266	4	AA839738 Human pro
20	49	48.5	277	4	AA880305 Human pro
21	49	48.5	277	4	AA880347 Human pro
22	49	48.5	288	4	AA880343 Human pro
23	49	48.5	289	4	AA841524 Human pro
24	49	48.5	304	3	AA857037 Human pro
25	49	48.5	519	6	AB020235 Protein e

26	48	47.5	296	4	ABG15624 Novel hum
27	48	47.5	547	6	ABM15867 Mycobacte
28	48	47.5	754	7	AD836201 Klebsiell
29	48	47.5	754	7	AD836160 Klebsiell
30	47.5	47.0	792	4	AA682199 S. epider
31	47.5	47.0	801	5	ABP40739 Staphyloc
32	47	46.5	117	6	ADA15777 Human GAG
33	47	46.5	117	6	ADP85417 Human GAG
34	47	46.5	510	8	ADQ08680 Clona int
35	47	46.5	1022	4	ABG02687 Novel hum
36	47	46.5	1278	6	ABG74682 Human CGD
37	47	46.5	2091	8	ADN61449 Human KXP
38	47	46.5	2193	6	ABR42219 Human pro
39	47	46.5	2219	8	ADN00364 Novel hum
40	47	46.5	2245	8	ADJ96651 Human Nim
41	46.5	46.0	571	7	ABO77402 Pseudomon
42	46	45.5	60	5	ABP34774 Human ORF
43	46	45.5	171	3	AA608178 Arabidops
44	46	45.5	197	3	AA608177 Arabidops
45	46	45.5	226	3	AA608176 Arabidops

ALIGNMENTS

RESULT 1	AA848327	standard; peptide; 20 AA.
ID	AA848327	
XX	AA848327:	
AC	20-APR-2001	(first entry)
DT	T. pallidum	acidic repeat protein immunogenic peptide arp 9.
DE	T. pallidum	acidic repeat protein immunogenic peptide arp 9.
XX	Treponema pallidum;	acidic repeat protein; arp; immunogenic; syphilis;
KM	yaws; bejel.	
XX	Treponema pallidum.	
OS	Treponema pallidum.	
XX	MO200077486-A2.	
PN	21-DEC-2000.	
XX	14-JUN-2000;	2000MO-US016425.
PF	14-JUN-1999;	99US-0138981P.
XX	14-JUN-1999;	99US-0138981P.
PR	(USSH)	US DEPT HEALTH & HUMAN SERVICES.
FA	Liu H. Steiner B, Rhodes B;	
XX	WPI; 2001-080711/09.	
DR	Detecting Treponema pallidum	in blood, saliva, etc., by detecting
XX	formation of a complex between	immunogenic peptides of acidic repeat
FT	protein of the bacterium and	an antibody present in the biological
PT	sample.	
XX	Claim 15; Fig 11; 73pp;	English.
PS	The invention relates to a	method of detecting presence of Treponema
XX	pallidum (Tp), anti-treponemal	antibodies (Abs), or both in a biological
CC	sample that involves contacting	an acidic repeat protein (arp), or one or
CC	more isolated immunogenic	TP peptides of arp with an Ab containing
CC	biological sample and then	detecting the formation of a complex between
CC	immunogenic peptides and	Ab. The presence of the complex indicates the
CC	presence of TP. The method	is thus useful for diagnosing syphilis, yaws,
CC	and bejel diseases. The	immunogenic peptides or the Abs raised against
CC	arp, as part of an immunogenic	composition, are useful for inducing a
CC	protective immune response	against syphilis, yaws or bejel caused by TP.
CC	Sequences AA848319-AA848330	represent immunogenic peptides of T. pallidum
CC	arp protein	

Jan 28 13:02:54 2005

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24 ; Search time 3.11606 Seconds

(without alignments)
617.555 Million cell updates/sec

Title: US-10-017-168-15

Perfect score: 101

Sequence: 1 EVEDVPKVEPASPAREGGER 20

Scoring table: ELOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	96.0	256	2 F71326	hypothetical prote
2	82	81.2	227	2 G71326	hypothetical prote
3	51.5	51.0	153	1 B69215	conserved hypothet
4	50	49.5	184	2 D84603	hypothetical prote
5	48	47.5	547	2 E70650	phosphoglucosylase
6	47	46.5	308	2 T17946	hypothetical prote
7	47	46.5	1151	2 T24541	hypothetical prote
8	46.5	46.0	946	2 D96503	protein F9C16.9 [I
9	46	45.5	437	2 C35147	integrase homolog
10	45	44.6	99	2 A55819	nonhistone chromos
11	45	44.6	178	2 E95994	hypothetical prote
12	45	44.6	264	1 G69884	conserved hypothet
13	45	44.6	798	2 T31022	hypothetical prote
14	45	44.6	873	2 T16282	hypothetical prote
15	45	44.6	1350	2 G36793	hypothetical prote
16	44	43.6	220	2 S26685	hypothetical prote
17	44	43.6	251	1 C36044	CAMP response elem
18	44	43.6	306	2 T00177	CAMP response elem
19	44	43.6	306	2 T00177	indole-3-glycerol-
20	44	43.6	306	2 G89988	hypothetical prote
21	44	43.6	344	2 JC5601	hypothetical prote
22	44	43.6	681	2 E81815	CAMP response elem
23	44	43.6	897	1 S22700	probable transpos
24	44	43.6	1069	2 E68202	amphiphysin chlc
25	44	43.6	1069	2 T00043	valine-tRNA ligase
26	44	43.6	1072	2 T00041	BH-protocadherin-a
27	44	43.6	1200	2 T00042	BH-protocadherin p
28	44	43.6	1537	2 JC4172	DNA (cytosine-5-)-
29	43	42.6	133	2 T36525	hypothetical prote

30	43	42.6	199	2 AB2847	conserved hypothet
31	43	42.6	210	2 C87305	hypothetical prote
32	43	42.6	217	2 C37944	CAMP response elem
33	43	42.6	220	2 A75287	response regulator
34	43	42.6	227	2 B97624	hypothetical prote
35	43	42.6	229	2 B37944	CAMP response elem
36	43	42.6	229	2 A37944	CAMP response elem
37	43	42.6	278	2 S36101	CAMP response elem
38	43	42.6	341	2 S20827	CAMP response elem
39	43	42.6	341	2 S26866	CAMP response elem
40	43	42.6	356	2 B71023	CAMP response elem
41	43	42.6	369	2 A39157	hypothetical prote
42	43	42.6	434	2 T47545	probable RNA helic
43	43	42.6	542	2 E84250	nondehydroascorba
44	43	42.6	668	1 COBEM1	acetyl-CoA synthet
45	43	42.6	670	1 YCNU	U52 protein - hum
					acetolactate synth

ALIGNMENTS

RESULT 1

F71326 hypothetical protein TP0433 - syphilis spirochete

C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C/Accession: F71326

R/Praser: C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi

erson, J.; Khalik, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McD

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A/Reference number: A71250; MUID:98332770; PMID:9665876

A/Accession: F71326

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-256 <COL>

A/Cross-references: UNIPROT:O83448; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AAC654

A/Experimental source: strain Nichols

C/Genetics:

A/Genes: TP0433

Query Match 96.0%; Score 97; DB 2; Length 256;

Best Local Similarity 95.0%; Pred. No. 3.8e-07;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVEDVPKVEPASPAREGGER 20

DB 184 EVEDVPKVEPASPAREGGER 203

RESULT 2

G71326 hypothetical protein TP0434 - syphilis spirochete

C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C/Accession: G71326

R/Praser: C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi

erson, J.; Khalik, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McD

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A/Reference number: A71250; MUID:98332770; PMID:9665876

A/Accession: G71326

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-227 <COL>

A/Cross-references: UNIPROT:O83449; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AAC654;

A/Experimental source: strain Nichols

C/Genetics:

A/Genes: TP0434

Query Match 81.2%; Score 82; DB 2; Length 227;

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 ; Search time 17.5517 seconds
(without alignments)

655,635 Million cell updates/sec

Title: US-10-017-168-15

Perfect score: 101

Sequence: 1 EVEDVPKVVPEPASPAREGGER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	348	2	Q9ALV7
2	101	100.0	393	2	Q93CA3
3	101	100.0	428	2	Q9ALV6
4	101	100.0	432	2	Q93CA4
5	101	100.0	548	2	Q93CA4
6	97	96.0	256	2	Q93CA4
7	82	81.2	227	2	Q93CA4
8	51.5	51.0	153	1	Y862_METTH
9	50	49.5	187	2	Q93CA3
10	50	48.5	193	2	Q93CA3
11	50	48.5	238	2	Q93CA3
12	50	48.5	238	2	Q93CA3
13	50	48.5	1174	2	Q93CA3
14	49	48.5	256	2	Q93CA3
15	48	47.5	482	2	Q93CA3
16	48	47.5	482	2	Q93CA3
17	48	47.5	547	2	Q93CA3
18	48	47.5	547	2	Q93CA3
19	48	47.5	2192	2	Q93CA3
20	47.5	47.0	792	2	Q93CA3
21	47	46.5	178	2	Q93CA3
22	47	46.5	178	2	Q93CA3
23	47	46.5	266	2	Q93CA3
24	47	46.5	280	2	Q93CA3
25	47	46.5	280	2	Q93CA3
26	47	46.5	308	2	Q93CA3
27	47	46.5	357	2	Q93CA3
28	47	46.5	357	2	Q93CA3
29	47	46.5	1159	2	Q93CA3
30	47	46.5	1165	2	Q93CA3
31	47	46.5	1165	2	Q93CA3

32	47	46.5	2297	1	MNK2_HUMAN
33	46.5	46.0	946	2	Q91P09
34	46	45.5	174	2	Q93CA3
35	46	45.5	200	2	Q93CA3
36	46	45.5	200	2	Q93CA3
37	46	45.5	290	2	Q93CA3
38	46	45.5	290	2	Q93CA3
39	46	45.5	348	2	Q93CA3
40	46	45.5	371	2	Q93CA3
41	46	45.5	383	2	Q93CA3
42	46	45.5	434	2	Q93CA3
43	46	45.5	434	2	Q93CA3
44	46	45.5	434	2	Q93CA3
45	46	45.5	437	1	INTR_SACER

ALIGNMENTS

RESULT 1

Q9ALV7 PRELIMINARY; PRT; 348 AA.

AC Q9ALV7
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Acidic repeat protein.

OS Treponema pallidum (subsp. pertenue) (Yaws treponeme).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=168;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=CDC2;
RA Liu H., Steiner B., Rodas B.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF342806; AAK01460.2; -
SQ SEQUENCE 348 AA; 37936 MW; EA4446BD2344592 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 348;
Best local similarity 100.0%; Pred. No. 6.2e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q9ALV7 1 EVEDVPKVVPEPASPAREGGER 20
DB 128 EVEDVPKVVPEPASPAREGGER 147

RESULT 2

Q93CA3 PRELIMINARY; PRT; 393 AA.

AC Q93CA3
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DE Acidic repeat protein.

OS Treponema pallidum (subsp. pertenue) (Yaws treponeme).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=168;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=CDC1;
RA Liu H., Steiner B.M., Rodas B.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411126; AAL07373.1; -
SQ SEQUENCE 393 AA; 42852 MW; C2D9198A1BB82B5 CRC64;

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 18.9507 Seconds
(without alignments)
378.592 Million cell updates/sec

Title: US-10-017-168-16

Perfect score: 101
Sequence: 1 EVENPKVPEPASEREGGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp19808:*
- 2: geneseqp19908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20038:*
- 8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	20	AA848328	T. pallid
2	101	100.0	432	AA848316	AA848316 T. pallid
3	96	95.0	20	AA848327	AA848327 T. pallid
4	96	95.0	232	AA848317	AA848317 T. pallid
5	96	95.0	312	AA848318	AA848318 T. pallid
6	92	91.1	20	AA848329	AA848329 T. pallid
7	82	81.2	20	AA848320	AA848320 T. pallid
8	77	76.2	20	AA848321	AA848321 T. pallid
9	77	76.2	20	AA848330	AA848330 T. pallid
10	65	64.4	21	AA848325	AA848325 T. pallid
11	55	54.5	19	AA848319	AA848319 T. pallid
12	53	52.5	26	AA848326	AA848326 T. pallid
13	53	52.5	754	AA848320	AA848320 T. pallid
14	53	52.5	754	AA848321	AA848321 T. pallid
15	50	49.5	79	AA848322	AA848322 T. pallid
16	50	49.5	187	AA848323	AA848323 T. pallid
17	50	49.5	187	AA848324	AA848324 T. pallid
18	50	49.5	754	AA848325	AA848325 T. pallid
19	50	49.5	754	AA848326	AA848326 T. pallid
20	50	49.5	754	AA848327	AA848327 T. pallid
21	50	49.5	754	AA848328	AA848328 T. pallid
22	50	49.5	754	AA848329	AA848329 T. pallid
23	50	49.5	754	AA848330	AA848330 T. pallid
24	50	49.5	754	AA848331	AA848331 T. pallid
25	50	49.5	754	AA848332	AA848332 T. pallid

26	50	49.5	754	7	AA848323	AA848323 T. pallid
27	50	49.5	754	7	AA848324	AA848324 T. pallid
28	50	49.5	754	7	AA848325	AA848325 T. pallid
29	50	49.5	754	7	AA848326	AA848326 T. pallid
30	50	49.5	754	7	AA848327	AA848327 T. pallid
31	50	49.5	754	7	AA848328	AA848328 T. pallid
32	50	49.5	754	7	AA848329	AA848329 T. pallid
33	50	49.5	754	7	AA848330	AA848330 T. pallid
34	50	49.5	754	7	AA848331	AA848331 T. pallid
35	50	49.5	754	7	AA848332	AA848332 T. pallid
36	48	47.5	211	6	AA848333	AA848333 T. pallid
37	48	47.5	211	6	AA848334	AA848334 T. pallid
38	48	47.5	296	4	AA848335	AA848335 T. pallid
39	48	47.5	307	6	AA848336	AA848336 T. pallid
40	47	46.5	170	6	AA848337	AA848337 T. pallid
41	47	46.5	266	4	AA848338	AA848338 T. pallid
42	47	46.5	266	4	AA848339	AA848339 T. pallid
43	47	46.5	266	4	AA848340	AA848340 T. pallid
44	47	46.5	277	4	AA848341	AA848341 T. pallid
45	47	46.5	277	4	AA848342	AA848342 T. pallid

ALIGNMENTS

RESULT 1	AA848328	standard; peptide: 20 AA.
XX	AA848328	
AC	AA848328	
XX	AA848328	
DT	20-APR-2001 (first entry)	
XX	20-APR-2001 (first entry)	
DE	T. pallidum acidic repeat protein immunogenic peptide arp 10.	
XX	Treponema pallidum, acidic repeat protein; arp; immunogenic; eyphills;	
KW	yaws; bejel.	
XX	Treponema pallidum.	
OS	MO200077486-A2.	
XX	MO200077486-A2.	
PD	21-DEC-2000.	
XX	21-DEC-2000.	
PF	14-JUN-2000; 2000WO-US016425.	
XX	14-JUN-2000; 2000WO-US016425.	
PR	14-JUN-1999; 99US-0138981P.	
XX	14-JUN-1999; 99US-0138981P.	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
PI	Liu H, Steiner B, Rhodes B;	
XX	Liu H, Steiner B, Rhodes B;	
DR	WPI; 2001-080711/09.	
XX	WPI; 2001-080711/09.	
PT	Detecting Treponema pallidum in blood, saliva, etc., by detecting	
PT	formation of a complex between immunogenic peptides of acidic repeat	
PT	protein of the bacterium and an antibody present in the biological	
PT	sample.	
XX	Claim 15, Fig 11; 73pp; English.	
PS	The invention relates to a method of detecting presence of Treponema	
XX	pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological	
CC	sample that involves contacting an acidic repeat protein (arp), or one or	
CC	more isolated immunogenic TP peptides of arp with an Ab containing	
CC	biological sample and then detecting the formation of a complex between	
CC	immunogenic peptides and Ab. The presence of the complex indicates the	
CC	presence of TP. The method is thus useful for diagnosing syphilis, yaws,	
CC	and bejel diseases. The immunogenic peptides or the Abs raised against	
CC	arp, as part of an immunogenic composition, are useful for inducing a	
CC	protective immune response against syphilis, yaws or bejel caused by TP.	
CC	Sequences AA848319-AA848330 represent immunogenic peptides of T. pallidum	
CC	arp protein	

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 ; Search time 17.5517 Seconds
(without alignments)

655.635 Million cell updates/sec

Title: US-10-017-168-16

Perfect score: 101

Sequence: 1 EVENPKVPEPASEREGGER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	432	2	051953
2	96	95.0	348	2	09ALV7
3	96	95.0	393	2	093CA3
4	96	95.0	428	2	09ALV6
5	96	95.0	548	2	093CA4
6	92	91.1	256	2	083448
7	78	77.2	227	2	083449
8	51	50.5	1174	2	062043
9	51	50.5	1174	2	BAC98029
10	50	49.5	187	2	09S1J8
11	50	49.5	193	2	0941I5
12	49.5	49.0	357	2	08PXY8
13	48	47.5	238	2	06ERF9
14	47	46.5	178	2	0700A7
15	47	46.5	178	2	CAG14963
16	47	46.5	256	2	08WV22
17	47	46.5	308	2	098494
18	47	46.5	357	2	06ZAE0
19	47	46.5	357	2	BAD03360
20	47	46.5	383	2	093CV7
21	47	46.5	1699	2	08UXI6
22	46.5	46.0	153	1	Y862 METTH
23	46	45.5	138	2	09FMV2
24	46	45.5	193	2	08POY1
25	46	45.5	250	2	078A15
26	46	45.5	348	2	08N446
27	46	45.5	435	1	ORCS_MOUSE
28	46	45.5	435	1	BAC39250
29	46	45.5	499	1	MPA2 ARATH
30	46	45.5	554	2	09JHT9
31	46	45.5	556	2	Q7SGY1

ALIGNMENTS

32	46	45.5	620	2	0923H2	Q523h2 mus musculus
33	46	45.5	710	2	08CHT1	Q8CHt1 mus musculus
34	46	45.5	756	2	075B14	Q75B14 ashbya gos
35	46	45.5	756	2	AAS51683	AAS51683 ashbya go
36	46	45.5	877	1	SYV METTH	Q56861 methanobact
37	46	45.5	1310	2	Q7PDP2	Q7Pdp2 plasmodium
38	46	45.5	1350	1	VG72 ICHV1	Q00103 ictaluxid h
39	46	45.5	1697	2	08JUG7	Q8Jjg7 normal-k-lik
40	46	45.5	1697	2	08JUL0	Q8Jjg7 normal-k-lik
41	46	45.5	2192	2	08IBW7	Q8IBw7 plasmodium
42	45.5	45.0	792	2	08CPY0	Q8Cpy0 staphylococ
43	45	44.6	119	2	06HPR8	Q6Hpr8 bacillus th
44	45	44.6	119	2	073FA6	Q73fa6 bacillus ce
45	45	44.6	119	2	Q81J50	Q81j50 bacillus ce

RESULT 1

ID	051953	PRELIMINARY;	PRT;	432 AA.
AC	051953;			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Acidic repeat protein.			
OS	Treponema pallidum.			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=160;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Nichols;			
RA	Steiner B.M., Liu H., Rodas B.;			
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF015824; AAB94541.1; -			
SO	SEQUENCE 432 AA; 46364 MW; 8PE1E4C55CE46A23 CRC64;			

Query Match 100.0%; Score 101; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	EVENPKVPEPASEREGGER 20
Db	228	EVENPKVPEPASEREGGER 247

RESULT 2

ID	09ALV7	PRELIMINARY;	PRT;	348 AA.
AC	09ALV7;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Acidic repeat protein.			
GN	Name=arp;			
OS	Treponema pallidum (subsp. pertenue) (Yaws treponeme).			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=168;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CDC2;			
RA	Liu H., Steiner B.;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CDC2;			
RA	Liu H., Steiner B.M., Rodas B.;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF342806; AAK01460.2; -			
SO	SEQUENCE 348 AA; 37936 MW; E4A446BD82344592 CRC64;			

Query Match 95.0%; Score 96; DB 2; Length 348;

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24 ; Search time 3.11606 Seconds
(without alignments)
617.555 Million cell updates/sec

Title: US-10-017-168-16

Perfect score: 101

Sequence: 1 EVENVPKXVEPASERREGGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 28316 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 28316

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	92	91.1	256 2	F71326 hypothetical prote
2	78	77.2	227 2	F71326 hypothetical prote
3	50	49.5	184 2	D84603 hypothetical prote
4	47	46.5	308 2	T17946 hypothetical prote
5	46.5	46.0	153 1	B69215 conserved hypote
6	46	45.5	897 2	B69202 valine-tRNA ligase
7	46	45.5	1350 2	G36793 hypothetical prote
8	45	44.6	220 2	S26885 CAMP response elem
9	45	44.6	344 2	JCS602 CAMP response elem
10	45	44.6	344 2	JCS601 CAMP response elem
11	45	44.6	682 1	S22700 amphiphysin - chic
12	44	43.6	178 2	E95994 CAMP response elem
13	44	43.6	217 2	C37944 CAMP response elem
14	44	43.6	229 2	B37944 CAMP response elem
15	44	43.6	229 2	A37944 CAMP response elem
16	44	43.6	278 2	S36101 CAMP response elem
17	44	43.6	312 2	E64072 CAMP response elem
18	44	43.6	341 2	S20827 spermidine/putresc
19	44	43.6	341 2	S26686 CAMP response elem
20	44	43.6	793 2	S67070 GAC1 protein - Yea
21	43	42.6	99 2	A55819 nonhistone chromos
22	43	42.6	135 2	S56887 histone H2B153 - w
23	43	42.6	275 2	F75102 hypothetical prote
24	43	42.6	289 2	T01257 probable GT-1-like
25	43	42.6	313 2	D86668 oligopeptide ABC t
26	43	42.6	315 2	D81131 hypothetical prote
27	43	42.6	356 2	B71023 hypothetical prote
28	43	42.6	382 2	T08301 hypothetical prote
29	43	42.6	547 2	E70650 phosphoglucomutase

30	43	42.6	554 2	B85015 hypothetical prote
31	43	42.6	559 2	T01724 hypothetical prote
32	43	42.6	566 2	T33926 hypothetical prote
33	43	42.6	1805 2	A34736 neatin - rat
34	42.5	42.1	272 2	B71618 mezoicite surface
35	42	41.6	345 2	A83526 hypothetical prote
36	42	41.6	369 2	A39157 probable RNA helic
37	42	41.6	463 2	T51194 hypothetical prote
38	42	41.6	490 2	E70649 probable regulator
39	42	41.6	623 2	G72412 hypothetical prote
40	42	41.6	688 2	B42161 cGMP-gated cation
41	42	41.6	1143 2	A87488 DNA polymerase III
42	42	41.6	1151 2	T24541 hypothetical prote
43	42	41.6	1272 2	C64513 hypothetical prote
44	42	41.6	1537 2	JC4172 DNA (cytosine-5')-
45	41.5	41.1	338 2	S78045 erythrocyte membra

ALIGNMENTS

RESULT 1

F71326 hypothetical protein TP0433 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_reviseion 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: F71326
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw
reton, U.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetereback, T.; Mc
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876

A:Accession: F71326

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-256 <COL>

A:Cross-references: UNIPROT:O83448; GB:AE001220; GB:AE000520; NID:g3322705; PIDN:AAC65

A:Experimental source: strain Nichols

C:Genetics:
A:Gene: TP0433

Query Match 91.1%; Score 92; DB 2; Length 256;
Best Local Similarity 90.0%; Pred. No. 1.6e-06;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVENVPKXVEPASERREGGER 20

DB 184 EVEDAPKXVEPASERREGGER 203

RESULT 2

G71326 hypothetical protein TP0434 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_reviseion 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: G71326

R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw
reton, U.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetereback, T.; Mc
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876

A:Accession: G71326

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-227 <COL>

A:Cross-references: UNIPROT:O83449; GB:AE001220; GB:AE000520; NID:g3322705; PIDN:AAC65

A:Experimental source: strain Nichols

C:Genetics:
A:Gene: TP0434

Query Match 77.2%; Score 78; DB 2; Length 227;

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 18.9507 Seconds
(without alignments)
378.592 Million cell updates/sec

Title: US-10-017-168-17

Perfect score: 101

Sequence: 1 EVEDAPKVEPASEREGGER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	20	4	AAB48329 T. pallid
2	101	100.0	432	4	AAB48316 T. pallid
3	97	96.0	20	4	AAB48327 T. pallid
4	97	96.0	232	4	AAB48317 T. pallid
5	97	96.0	312	4	AAB48318 T. pallid
6	92	91.1	20	4	AAB48328 T. pallid
7	91	90.1	20	4	AAB48320 T. pallid
8	78	77.2	20	4	AAB48330 T. pallid
9	77	76.2	20	4	AAB48321 T. pallid
10	65	64.4	21	4	AAB48325 T. pallid
11	64	63.4	19	4	AAB48319 T. pallid
12	53	52.5	26	4	AAB48326 T. pallid
13	48	47.5	296	4	ABG15624 Novel hum
14	47	46.5	79	3	AAAG1691 Arabidops
15	47	46.5	187	3	AAAG1629 Arabidops
16	47	46.5	187	3	AAAG1629 Arabidops
17	47	46.5	434	3	AAAG1629 Arabidops
18	47	46.5	434	3	AAAG1629 Arabidops
19	47	46.5	434	3	AAAG1629 Arabidops
20	47	46.5	434	3	AAAG1629 Arabidops
21	47	46.5	612	3	AAAG1629 Arabidops
22	46	45.5	763	3	AAAG1629 Arabidops
23	46	45.5	437	4	ABM15867 Mycobacte
24	46	45.5	547	6	ABM15867 Mycobacte
25	46	45.5	571	7	ABO77402 Pseudomon

ALIGNMENTS

26	46	45.5	1007	4	AAB50660	AAB50660 C. elegan
27	46	45.5	1226	3	AAAG4239	AAAG4239 Arabidops
28	46	45.5	1321	3	AAAG4238	AAAG4238 Arabidops
29	46	45.5	1351	3	AAAG4237	AAAG4237 Arabidops
30	45	44.6	109	4	AAU40366	AAU40366 Propionib
31	45	44.6	109	6	ABM36885	ABM36885 Murine BH
32	45	44.6	170	6	ADAS5215	ADAS5215 Human pro
33	45	44.6	266	4	AAAB80279	AAAB80279 Human pro
34	45	44.6	266	4	AAAB80279	AAAB80279 Human pro
35	45	44.6	266	4	AAAB80279	AAAB80279 Human pro
36	45	44.6	277	4	AAAB80305	AAAB80305 Human pro
37	45	44.6	277	4	AAAB80347	AAAB80347 Human pro
38	45	44.6	288	4	AAAB80343	AAAB80343 Human pro
39	45	44.6	289	4	AAAB80343	AAAB80343 Human pro
40	45	44.6	304	3	AAAB57037	AAAB57037 Human pro
41	45	44.6	510	8	ADQ08680	ADQ08680 Clona. int
42	45	44.6	519	6	ABU20235	ABU20235 Murine BH
43	45	44.6	944	4	ABM60979	ABM60979 Drosophill
44	45	44.6	1841	2	AAW22605	AAW22605 Ty lactone
45	45	44.6	1841	2	AAW22605	AAW22605 Ty lactone

RESULT 1

AAB48329 standard; peptide: 20 AA.

AAB48329;

20-Apr-2001 (first entry)

T. pallidum acidic repeat protein immunogenic peptide arp 11.

Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;

yaws; bejel.

Treponema pallidum.

W0200077486-A2.

14-JUN-2000; 2000MO-US016425.

14-JUN-1999; 99US-0138981P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Liu H, Steiner B, Rhodes B;

WPI; 2001-080711/09.

Detecting Treponema pallidum in blood, saliva, etc., by detecting

formation of a complex between immunogenic peptides of acidic repeat

protein of the bacterium and an antibody present in the biological

sample.

Claim 15; Fig 11; 73pp; English.

The invention relates to a method of detecting presence of Treponema

pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological

sample that involves contacting an acidic repeat protein (arp), or one or

more isolated immunogenic TP peptides of arp with an Ab containing

biological sample and then detecting the formation of a complex between

immunogenic peptides and Ab. The presence of the complex indicates the

presence of TP. The method is thus useful for diagnosing syphilis, yaws,

and bejel diseases. The immunogenic peptides or the Abs raised against

arp, as part of an immunogenic composition, are useful for inducing a

protective immune response against syphilis, yaws or bejel caused by TP.

Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum

arp protein

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24 ; Search time 3.11606 Seconds
(without alignments)
617.555 Million cell updates/sec

Title: US-10-017-168-17

Perfect score: 101
Sequence: 1 EVEDAPKVEPASEREGGER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	256	2 F71326	hypothetical prote
2	78	77.2	227	2 G71326	hypothetical prote
3	51	50.5	1151	2 T24541	hypothetical prote
4	47.5	47.0	153	1 B69215	conserved hypotnet
5	47	46.5	184	2 D84603	hypothetical prote
6	47	46.5	210	2 C87305	hypothetical prote
7	47	46.5	434	2 T47545	monodehydroascorba
8	47	46.5	668	1 QOBEW1	US2 protein - hum
9	46	45.5	428	2 T32952	hypothetical prote
10	46	45.5	547	2 E70650	phosphoglucosyltrans
11	46	45.5	1408	2 T47671	P-91glycoprotein-11k
12	45	44.6	133	2 T36525	hypothetical prote
13	45	44.6	382	2 T08301	hypothetical prote
14	44.5	44.1	467	2 AH3437	DNA repair protein
15	44	43.6	82	1 QPBO	micro glutamic aci
16	44	43.6	168	1 T22246	response regulator
17	44	43.6	220	2 A75287	hypothetical prote
18	44	43.6	297	2 F70572	hypothetical prote
19	44	43.6	437	2 C35147	integrase homolog
20	44	43.6	1106	1 TVHUGL	transforming prote
21	43	42.6	133	2 T07910	hypothetical prote
22	43	42.6	306	2 T00177	hypothetical prote
23	43	42.6	306	2 G89988	hypothetical prote
24	43	42.6	308	2 T17946	hypothetical prote
25	43	42.6	356	2 B71023	hypothetical prote
26	43	42.6	357	2 H71122	hypothetical prote
27	43	42.6	414	2 A69866	3-oxoacyl-[acyl]-ca
28	43	42.6	542	2 E84250	acetyl-CoA synthet
29	43	42.6	852	2 T06310	hypothetical prote

30	43	42.6	1135	2 T30561	Scythe protein - A
31	42.5	42.1	525	2 JN0443	transcription init
32	42.5	42.1	946	2 D96503	protein P9C16.9 (i
33	42.5	42.1	2149	2 T47655	hypothetical prote
34	42	41.6	135	2 S56687	histone H2B153 - w
35	42	41.6	223	2 JX0222	ubiquitin thiolest
36	42	41.6	463	2 T51194	hypothetical prote
37	42	41.6	554	2 JMW094	neurofilament prot
38	42	41.6	733	2 S23468	ococyte-specific pr
39	42	41.6	925	2 G88175	protein T24H7.2 (i
40	42	41.6	1032	2 D83637	serine/threonine p
41	42	41.6	1076	2 S44764	C27D11.1 protein -
42	42	41.6	1272	2 C64513	hypothetical prote
43	42	41.6	1350	2 G36793	hypothetical prote
44	41	40.6	73	2 S59954	ribosomal protein
45	41	40.6	99	2 A53819	nonhistone chromos

ALIGNMENTS

RESULT 1

F71326
hypothetical protein TP0433 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: F71326
R/Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; Mc
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; MUID:98332770; PMID:9665876
A/Accession: F71326
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-256 <COL>
A/Cross-references: UNIPROT:O83448; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AC65
A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0433

Query Match 100.0%; Score 101; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVEDAPKVEPASEREGGER 20

DB 184 EVEDAPKVEPASEREGGER 203

RESULT 2

G71326
hypothetical protein TP0434 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: G71326
R/Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; Mc
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; MUID:98332770; PMID:9665876
A/Accession: G71326
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-227 <COL>
A/Cross-references: UNIPROT:O83449; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AC65
A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0434

Query Match 77.2%; Score 78; DB 2; Length 227;

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 ; Search time 17.5517 Seconds
(without alignments)
655.635 Million cell updates/sec

Title: US-10-017-168-17
Perfect score: 101
Sequence: 1 EVEDAPKVEBPASEREGGER 20

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Uniprot 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	256	2	083448
2	101	100.0	432	2	051953
3	101	100.0	548	2	093CA4
4	97	96.0	348	2	093CA4
5	97	96.0	393	2	093CA3
6	97	96.0	428	2	093CA3
7	97	96.0	428	2	093CA3
8	97	96.0	428	2	093CA3
9	51	50.5	1165	2	070KPE
10	51	50.5	1165	2	070KPE
11	50	49.5	434	2	075UW6
12	50	49.5	434	2	093X74
13	50	49.5	434	2	093X74
14	50	49.5	434	2	093X74
15	49	48.5	151	2	084851
16	49	48.5	151	2	084851
17	49	48.5	294	2	060UG2
18	48	47.5	769	2	075BK7
19	48	47.5	769	2	075BK7
20	48	47.5	769	2	075BK7
21	47.5	47.0	153	2	081D12
22	47.5	47.0	153	2	081D12
23	47	46.5	130	2	08CC10
24	47	46.5	168	2	08LH12
25	47	46.5	187	2	0981J8
26	47	46.5	193	2	0941I5
27	47	46.5	210	2	094A20
28	47	46.5	344	2	098H20
29	47	46.5	357	2	062AE0
30	47	46.5	357	2	062AE0
31	47	46.5	612	2	09VG45

ALIGNMENTS

32	47	46.5	612	2	096019	Q96019 drosophila
33	47	46.5	668	1	U152_HCMVA	P16793 human cytom
34	47	46.5	668	2	07M6N1	Q7M6N1 human cytom
35	47	46.5	668	2	AAA46006	AAA46006 human cyr
36	47	46.5	1174	2	062Q43	Q62Q43 mus muscu
37	47	46.5	1174	2	BAC98029	BAC98029 mus muscu
38	47	46.5	1475	2	06CBP1	Q6CBP1 yarrowia 11
39	46	45.5	238	2	06ERF9	Q6ERF9 oryza sativ
40	46	45.5	261	2	090UP7	Q90UP7 mus muscu
41	46	45.5	262	2	075Z26	Q75Z26 sus scrofa
42	46	45.5	262	2	088346	Q88346 sus muscu
43	46	45.5	262	2	BAC82459	BAC82459 sus scro
44	46	45.5	295	2	Q890S6	Q890S6 clostridium
45	46	45.5	547	2	P95090	P95090 mycobacteri

RESULT 1

ID	083448	PRELIMINARY;	PRT;	256 AA.
AC	083448:			
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	Hypothetical protein TP0433.			
GN	OrderedLocustNames=TP0433;			
OS	Treponema pallidum.			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=160;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Nichols;			
RX	MEDLINE=98133770; PubMed=9665876;			
RA	Fraser C.M., Norris S.D., Weinstein G.M., White O., Sutton G.G.,			
RA	Dodson R.J., Gwinn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,			
RA	Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,			
RA	Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,			
RA	Uterback T.R., McDonald L.A., Artlich P., Bowman C., Cotton M.D.,			
RA	Fuili C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,			
RA	Weldman J.F., Smith H.O., Venter J.C.;			
RT	"Complete genome sequence of Treponema pallidum, the syphilis			
RT	spirochete.";			
RL	Science 281:375-388(1998).			
DR	EMBL; AE001220; AAC65421.1; -			
DR	PIR; F71326; F71326.			
DR	TIGR; TP0433; -			
KW	Complete proteome; Hypothetical protein.			
SQ	SEQUENCE 256 AA; 27453 MW; E90329D25A119E76 CRC64;			
QY	Query Match	100.0%;	Score 101;	DB 2; Length 256;
	Best Local Similarity	100.0%;	Pred. No. 8.1e-07;	
DB	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
	1 EVEDAPKVEBPASEREGGER 20			
	184 EVEDAPKVEBPASEREGGER 203			
RESULT 2				
ID	051953	PRELIMINARY;	PRT;	432 AA.
AC	051953:			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Acidic repeat protein.			
OS	Treponema pallidum.			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=160;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 18.9507 Seconds
(without alignments)
378.592 Million cell updates/sec

Title: US-10-017-168-18

Sequence: 1 EVEDVGVGVPAAGSGEGGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	106	100.0	20 4 AAB48330	Aab48330 T. pallid
2	106	100.0	432 4 AAB48316	Aab48316 T. pallid
3	82	77.4	20 4 AAB48327	Aab48327 T. pallid
4	82	77.4	232 4 AAB48317	Aab48317 T. pallid
5	82	77.4	312 4 AAB48318	Aab48318 T. pallid
6	78	73.6	20 4 AAB48329	Aab48329 T. pallid
7	77	72.6	20 4 AAB48328	Aab48328 T. pallid
8	69	65.1	26 4 AAB48326	Aab48326 T. pallid
9	68	64.2	20 4 AAB48320	Aab48320 T. pallid
10	58	54.7	20 4 AAB48321	Aab48321 T. pallid
11	55	51.9	754 7 ADE36201	Ade36201 Klebsiell
12	55	51.9	754 7 ADE36160	Ade36160 Klebsiell
13	53	50.0	19 4 AAB48319	Aab48319 T. pallid
14	53	50.0	21 4 AAB48325	Aab48325 T. pallid
15	52	49.1	211 6 AAB64080	Aab64080 Propionib
16	52	49.1	307 6 AAB66113	Aab66113 Propionib
17	52	49.1	754 7 ADE36210	Ade36210 Klebsiell
18	52	49.1	754 7 ADE36219	Ade36219 Klebsiell
19	52	49.1	754 7 ADE36207	Ade36207 Klebsiell
20	52	49.1	754 7 ADE36198	Ade36198 Klebsiell
21	52	49.1	754 7 ADE36222	Ade36222 Klebsiell
22	52	49.1	754 7 ADE36228	Ade36228 Klebsiell
23	52	49.1	754 7 ADE36163	Ade36163 Klebsiell
24	52	49.1	754 7 ADE36204	Ade36204 Klebsiell
25	52	49.1	754 7 ADE36204	Ade36204 Klebsiell

26	52	49.1	754 7 ADE36234	Ade36234 Klebsiell
27	52	49.1	754 7 ADE36216	Ade36216 Klebsiell
28	52	49.1	754 7 ADE36249	Ade36249 Klebsiell
29	52	49.1	754 7 ADE36213	Ade36213 Klebsiell
30	52	49.1	754 7 ADE36237	Ade36237 Klebsiell
31	52	49.1	754 7 ADE36225	Ade36225 Klebsiell
32	52	49.1	754 7 ADE36240	Ade36240 Klebsiell
33	52	49.1	754 7 ADE36246	Ade36246 Klebsiell
34	52	49.1	754 7 ADE36231	Ade36231 Klebsiell
35	52	49.1	754 7 ADE36243	Ade36243 Klebsiell
36	51.5	48.6	228 7 ABO84152	Abo84152 Pseudom
37	50.5	47.6	76 4 ABO60228	Abo60228 Propionib
38	50.5	47.6	76 6 ABO65747	Abo65747 Propionib
39	50	47.2	340 8 ADNA6982	Adna6982 Thermococ
40	50	47.2	350 6 ABUD6303	Abud6303 Protein e
41	50	47.2	394 7 ABO79086	Abo79086 Pseudom
42	50	47.2	1504 7 ABO77862	Abo77862 Pseudom
43	49.5	46.7	683 7 ADNA4887	Adna4887 Rat Prote
44	49	46.2	19938 6 ABP76679	Abp76679 Streptomy
45	48.5	45.8	2044 4 ABB61488	Abb61488 Drosophi1

ALIGNMENTS

RESULT 1
AAB48330
ID AAB48330 standard; peptide; 20 AA.
XX
AC AAB48330;
XX
DT 20-APR-2001 (first entry)
XX
DE T. pallidum acidic repeat protein immunogenic peptide a:rp 12.
XX
KM Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW yaws; bejel.
XX
OS Treponema pallidum.
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016425.
XX
PR 14-JUN-1999; 99US-0138981P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;
XX
DR WPI, 2001-080711/09.
XX
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample.
XX
PS Claim 15, Fig 11, 73pp, English.
XX
XX
XX The invention relates to a method of detecting presence of Treponema
XX pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
XX sample that involves contacting an acidic repeat protein (arp), or one or
XX more isolated immunogenic TP peptides of arp with an Ab containing
XX immunogenic peptides and then detecting the formation of a complex between
XX immunogenic peptides and Ab. The presence of the complex indicates the
XX presence of TP. The method is thus useful for diagnosing syphilis, yaws,
XX and bejel diseases. The immunogenic peptides or the Abs raised against
XX arp, as part of an immunogenic composition, are useful for inducing a
XX protective immune response against syphilis, yaws or bejel caused by TP.
XX Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
XX arp protein

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 Search time 17.5517 Seconds
(without alignment)
655.635 Million cell updates/sec

Title: US-10-017-168-18

Perfect score: 106

Sequence: 1 EVEDVPGVPEPASGHEGGER 20

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter 45 summaries

Database: UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

1	106	100.0	227	2	083449	083449 treponema p
2	106	100.0	432	2	051953	051953 treponema p
3	106	100.0	548	2	093C4	093C4 treponema p
4	82	77.4	348	2	09ALV7	09ALV7 treponema p
5	82	77.4	393	2	093CA3	093CA3 treponema p
6	82	77.4	428	2	09ALV6	09ALV6 treponema p
7	78	73.6	256	2	083448	083448 treponema p
8	57	53.8	213	2	07U803	07U803 treponema p
9	55	51.9	408	2	08X238	08X238 treponema p
10	54	50.9	756	2	075B14	075B14 ashbya goss
11	54	50.9	756	2	AAS51683	AAS51683 ashbya goss
12	53	50.0	370	1	V2R_PIG	V2R_PIG sus scrofa
13	53	50.0	378	1	MSAB_VIRCH	MSAB_VIRCH v peptide m
14	53	50.0	516	2	082N2	082N2 streptomyces
15	51	48.1	370	1	VB11_HAANI	VB11_HAANI halobacteri
16	51	48.1	380	2	087JFI	087JFI rhizobium m
17	50	47.2	198	1	MSA2_RHIME	MSA2_RHIME rhizobium m
18	50	47.2	347	2	07VK84	07VK84 helicobacte
19	50	47.2	350	2	09PJ30	09PJ30 campylobact
20	50	47.2	524	2	08LSK4	08LSK4 phycomitrite
21	49.5	46.7	683	1	AMPH_RAT	AMPH_RAT ratius novy
22	49	46.2	226	2	07U7G3	07U7G3 synecococc
23	49	46.2	358	2	07X284	07X284 streptomyces
24	49	46.2	1165	2	07JUK6	07JUK6 caenorhabd
25	49	46.2	1165	2	CAF31485	CAF31485 caenorhabd
26	48.5	45.8	365	2	08NIM9	08NIM9 aspergillus
27	48.5	45.8	373	2	08HMI1	08HMI1 oryza sativ
28	48.5	45.8	2044	1	SIF2_DROME	SIF2_DROME drosophila
29	48.5	45.8	2052	2	09VNR8	09VNR8 drosophila
30	48.5	45.8	2061	2	08MT93	08MT93 drosophila
31	48.5	45.8	2061	2	AAS65075	AAS65075 drosophila

32	48.5	45.8	2064	1	SIF1_DROME	SIF1_DROME drosophila
33	48.5	45.8	2072	2	09VNR7	09VNR7 drosophila
34	48	45.3	260	2	0985K8	0985K8 rhizobium l
35	48	45.3	325	2	09RSY7	09RSY7 detinococcus
36	48	45.3	416	2	076L87	076L87 oryzae lat
37	48	45.3	416	2	BAD00703	BAD00703 oryzae lat
38	48	45.3	417	2	089VE2	089VE2 bradyrhizob
39	48	45.3	919	2	06NZL0	06NZL0 mus musculu
40	48	45.3	919	2	AAH66079	AAH66079 mus musculu
41	47.5	44.8	2000	2	09Y410	09Y410 homo sapien
42	47	44.3	155	2	082RZ6	082RZ6 nitrosomona
43	47	44.3	160	2	08H6T1	08H6T1 chlamydomon
44	47	44.3	196	1	MSA2_CAUCR	MSA2_CAUCR cauliobacter
45	47	44.3	227	2	0820D6	0820D6 streptomyces

ALIGNMENTS

RESULT 1	083449	PRELIMINARY:	PRT:	227 AA.
ID	083449			
AC	083449			
DT	01-NOV-1998	(TREMBLrel. 08, Created)		
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)		
DE	Hypothetical protein TP0434.			
GN	OrderedlocusNames=TP0434;			
OS	Treponema pallidum			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=160;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	STRAIN=Nichols;			
RX	MEDLINE=98332770; PubMed=9665876;			
RA	Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,			
RA	Dodson R.J., Gwinn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,			
RA	Sodergren E., Hardham J.M., McLeod M.P., Salberg S.L., Peterson J.D.,			
RA	Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,			
RA	Utterback T.R., McDonald L.A., Artlich P., Bowman C., Cotton M.D.,			
RA	Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,			
RA	Weldman J.F., Smith H.O., Venter J.C.;			
RT	"Complete genome sequence of Treponema pallidum, the hyphills			
RT	spirochete."			
RL	Science 281:375-388(1998).			
DR	EMBL; AEO01220; AAC65422.1; -			
DR	PIR; G71326; G71326.			
DR	TIGR; TP0434;			
KW	Complete proteome; Hypothetical protein.			
SQ	SEQUENCE 227 AA; 25035 MW; 3FA02711A86E45FE CRC64;			
Query Match	100.0%; Score 106; DB 2; Length 227;			
Best Local Similarity	100.0%; Pred. No. 1.8e-07;			
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 EVEDVPGVPEPASGHEGGER 20			
Db	47 EVEDVPGVPEPASGHEGGER 66			
RESULT 2	051953	PRELIMINARY:	PRT:	432 AA.
ID	051953			
AC	051953			
DT	01-JUN-1998	(TREMBLrel. 06, Created)		
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)		
DT	01-OCT-2002	(TREMBLrel. 22, Last annotation update)		
DE	Acidic repeat protein.			
OS	Treponema pallidum			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=160;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 7357.76 Seconds
(without alignments)
10846.472 Million cell updates/sec

Title: US-10-017-168-19

Perfect score: 1647

Sequence: 1 atgtctgtcgcgcagtcgacat.....ttctgaaagcgcgcatga 1647

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_pn.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1647	100.0	1647	1	AF411124 Treponema
2	1634.4	99.2	2945	6	AX068032 Sequence
3	1634.4	99.2	2946	1	AF015824 Treponema
4	909	55.2	1287	1	AF342807 Treponema
5	858.4	52.1	939	6	AX068036 Sequence
6	823.2	50.0	14268	1	AE001220 Treponema
7	788	47.8	1182	1	AF411126 Treponema
8	653	39.6	1047	1	AF342806 Treponema
9	621.6	37.7	699	6	AX068034 Sequence
10	248.6	15.1	197411	10	AC135961 Treponema
11	245.6	14.9	211580	2	AC111089 Mus muscu
12	244.2	14.8	178257	10	AC123509 Mus muscu
13	235	14.3	144093	10	AC108193 Mus muscu
14	234.6	14.2	205054	10	AC098712 Mus muscu
15	233.8	14.2	179206	2	AC124108 Mus muscu
16	233.8	14.2	200574	10	BX005304 Mouse DNA
17	231.8	14.1	124244	10	AL929026 Mouse DNA
18	231.8	14.1	178620	10	AC121865 Mus muscu
19	231	14.0	110000	2	AC120236 Rattus no

20	231	14.0	152618	10	AC127583
21	230.2	14.0	165582	10	AC122020 Mus muscu
22	230.2	14.0	194387	10	AC105989 Mus muscu
23	230.2	14.0	194736	10	AC126271 Mus muscu
24	228.4	13.9	120487	10	AC103637 Mus muscu
25	227	13.8	199378	2	AC108256 Rattus no
26	226.8	13.8	171593	10	AC122052 Mus muscu
27	226.6	13.8	152435	10	AC121566 Mus muscu
28	225.8	13.7	237814	10	AC091464 Mus muscu
29	225.4	13.7	187287	10	AL928735 Mouse DNA
30	223.6	13.6	240931	2	AC107097 Rattus no
31	223.2	13.6	76941	10	BX000698 Mouse DNA
32	223.2	13.6	157754	10	AC132313 Mus muscu
33	221.8	13.5	187126	10	AC133115 Mus muscu
34	221.4	13.4	97839	2	AC141520 Rattus no
35	221.4	13.4	215745	10	AC117585 Mus muscu
36	221.4	13.4	234888	2	AC102097 Mus muscu
37	220.6	13.4	195690	10	AC098726 Mus muscu
38	220.2	13.4	157152	10	AC114679 Mus muscu
39	216.4	13.1	169003	10	AC115699 Mus muscu
40	216.2	13.1	178501	10	AC121862 Mus muscu
41	214.8	13.0	260625	2	AC096018 Rattus no
42	214.2	13.0	248718	10	AC117629 Mus muscu
43	213.8	13.0	217353	10	AC149611 Mus muscu
44	212.8	12.9	211947	10	AC107828 Mus muscu
45	212.6	12.9	171570	10	AL807807 Mouse DNA

ALIGNMENTS

RESULT 1
AF411124 1647 bp DNA linear BCF 26-SEP-2001
LOCUS Treponema pallidum subsp. pallidum strain Nichols acidic repeat
DEFINITION protein (arp) gene, complete cds.

ACCESSION AF411124.1 GI:15778312

VERSION AF411124

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

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REFERENCE

FEATURES
source
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/strain="Nichols"
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/protein_id="AA07372.1"
/db_xref="GI:15778313"
/translation="MFRSDMFPKTAVERISNLEKNAQAQAVVIGHAGIPGLLVSLAP
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AGHTVEYRDTVPFDPRLVSPSRVEDAPKVEPASREGEERVEDAPKVEPAS
EREGREVEDVPKVEPASREGEERVEDAPKVEPASREGEERVEDVPKVEP

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 929.12 Seconds

(without alignments)
10493.597 Million cell updates/sec

Title: US-10-017-168-19

Perfect score: 1647

Sequence: 1 atgcttctgcgcagtcacat.....ttctgaaagcgcatga 1647

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn190s:*
- 3: Geneseqn200s:*
- 4: Geneseqn201as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2003bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2003ds:*
- 11: Geneseqn2004as:*
- 12: Geneseqn2004bs:*
- 13: Geneseqn2004cs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1634.4	99.2	2945	4	AAC84647
2	858.4	52.1	939	4	AAC84649
3	695.8	42.2	9410	2	AAX20603
4	621.6	37.7	699	4	AAC84648
5	206.4	12.5	1926	10	ADK65580
6	206.2	12.5	1926	3	AAAS0254
7	206.2	12.5	1926	4	AAAF82902
8	206.2	12.5	2580	3	AAAF75454
9	206.2	12.5	2580	6	AAI64275
10	206.2	12.5	5452	2	AAAX90923
11	206.2	12.5	8705	12	AAZ23778
12	206.2	12.5	9480	12	ADP64415
13	206.2	12.5	9600	6	AAV21683
14	206.2	12.5	10285	6	ABST1027
15	206.2	12.5	10285	6	ABST6453
16	206.2	12.5	10330	12	ADL67154
17	206.2	12.5	10380	2	AAZ22248
18	206.2	12.5	10477	12	ADL67152
19	206.2	12.5	10516	12	ADL67150
20	206.2	12.5	10516	12	ADL67150

ALIGNMENTS

C	21	206.2	12.5	10561	12	ADL67148	AdL67148 Plasmid P
C	22	206.2	12.5	10596	2	AAQ51731	AaQ51731 Plasmid P
C	23	206.2	12.5	10596	2	AAAX15650	AaX15650 Nucleoid
C	24	206.2	12.5	10596	2	AAAT0348	AaT0348 Plasmid P
C	25	206.2	12.5	10615	12	ADL67175	AdL67175 Plasmid P
C	26	206.2	12.5	10774	12	ADL67153	AdL67153 Plasmid P
C	27	206.2	12.5	10921	12	ADL67151	AdL67151 Plasmid P
C	28	206.2	12.5	10961	12	ADL67149	AdL67149 Plasmid P
C	29	206.2	12.5	11006	12	ADL67147	AdL67147 Plasmid P
C	30	206.2	12.5	11059	12	ADL67176	AdL67176 Plasmid P
C	31	206.2	12.5	11693	13	ADL12379	AdL12379 Vector PC
C	32	206.2	12.5	11924	12	ADP007395	AdP007395 Modified
C	33	206.2	12.5	12242	12	ADP007394	AdP007394 Modified
C	34	206.2	12.5	16080	3	AAAS9553	AaAS9553 DNA clone
C	35	206.2	12.5	17753	12	ADL71910	AdL71910 Expression
C	36	206.2	12.5	17281	12	ADN12161	AdN12161 Epsstein-B
C	37	203.6	12.4	12733	6	ABK98631	AbK98631 Vector PE
C	38	203.6	12.4	12733	9	ACD13882	AcD13882 L. lactis
C	39	203.6	12.4	12739	6	ABK98592	AbK98592 Vector PE
C	40	203.6	12.4	12739	9	ACD13843	AcD13843 Plasmid P
C	41	202	12.3	30191	12	ADQ97654	AdQ97654 Mouse can
C	42	199.8	12.1	1925	2	AAAX90924	AaX90924 Epsstein B
C	43	191.2	11.6	799	2	AAV55831	AaV55831 Nucleoid
C	44	177.8	10.8	795	2	AAV55830	AaV55830 FlGA Inse
C	45	163.8	9.9	3127	12	ADN12154	AdN12154 Kaposi's s

RESULT 1

AA84647	standard; DNA; 2945 BP.
AA84647	
AC	AA84647;
XX	
DT	11-SEP-2003 (revised)
DT	20-APR-2001 (first entry)
XX	
DE	T. pallidum acidic repeat protein (arp) encoding DNA.
XX	
KW	Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW	yaws; bejel; de.
XX	
OS	Treponema pallidum; ssp. pallidum.
XX	
FH	Key location/Qualifiers
FT	CDS 919..2217
FT	/*tag= a
XX	
XX	WO200077486-A2.
XX	
PD	21-DEC-2000.
XX	
PF	14-JUN-2000; 2000WC-US016425.
XX	
PR	14-JUN-1999; 99US-0138981P.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Liu H, Steiner B, Rhodes B;
XX	
DR	WPI; 2001-080711/09.
XX	P-PSDB; AAB48316.
PT	Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT	formation of a complex between immunogenic peptides of acidic repeat
PT	protein of the bacterium and an antibody present in the biological
PT	sample.
XX	
PS	Claim 19; Fig 5; 73pp; English.
XX	
CC	The invention relates to a method of detecting presence of Treponema